

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:48:48 ; Search time 3017 Seconds
(without alignments)
8817.612 Million cell updates/sec

Title: US-10-327-713-267

Perfect score: 468
Sequence: 1 gacgcagctgcgcctcagctg.....ngncacaccgcgcctcagc 468

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

GenBank:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415	88.7	2962	9 BC015301	Mus muscu
2	378.2	80.8	2851	8 BC085781	Rattus no
3	316	67.5	2308	8 AK222911	Homo sapi
4	316	67.5	2392	8 AK831134	Sequence
5	316	67.5	2392	8 AK094636	Homo sapi
6	316	67.5	2417	6 CQ717207	Sequence
7	316	67.5	2487	6 BD156975	Primer fo
8	316	67.5	2487	6 AX878013	Sequence
9	316	67.5	2487	8 AK002018	Homo sapi
10	316	67.5	5089	6 CQ850926	Sequence
11	316	67.5	5089	8 AK128129	Homo sapi
12	312.8	66.8	2417	8 AF047690	Homo sapi
13	302.4	64.6	2383	6 BD160664	Sequence
14	302.4	64.6	2383	6 AX884014	Sequence
15	302.4	64.6	2383	8 AK024401	Homo sapi
16	231	49.4	2199	8 AK094005	Homo sapi
17	186.2	39.8	744	6 BD150403	Primer fo
18	186.2	39.8	744	6 AX870341	Sequence

19	149.4	31.9	2625	5 BC092161	Danio rer
20	147.8	31.6	182659	9 AC120353	Mus muscu
21	147.8	31.6	185733	9 AC113055	Mus muscu
22	142.6	30.5	254	10 G30716	Br
23	130.4	27.9	187322	14 AC122993	Rattus no
24	130.4	27.9	220259	14 AC134763	Rattus no
25	130.4	27.9	226877	14 AC097312	Rattus no
26	130.4	27.9	254629	14 AC133227	Rattus no
27	119.4	25.5	181369	8 AC146440	Pan trogl
28	119.4	25.5	241515	14 AC147287	Pan trogl
29	116.2	24.8	213045	14 AC093460	Homo sapi
30	116.2	24.8	216408	14 AC092466	Homo sapi
31	116.2	24.8	222605	8 AC010973	Homo sapi
32	111.8	23.9	861	10 BV102674	MARC 1563
33	93	19.9	2379	6 CQ574749	Sequence
34	93	19.9	2539	2 AY118801	Drosophi1
35	93	19.9	4940	6 CQ574748	Sequence
36	93	19.9	74697	14 AC020500	Drosophi1
37	93	19.9	153733	2 AC023681	Drosophi1
38	93	19.9	172105	2 AC104625	Drosophi1
39	93	19.9	172105	2 AC104625	Drosophi1
40	88	18.8	662	6 BD149815	Primer fo
41	88	18.8	662	6 AX869753	Sequence
42	73.8	15.8	225119	14 AC015894	Homo sapi
43	67	14.3	225119	14 AC015894	Homo sapi
44	51.8	11.1	1647	6 AR622810	Sequence
45	51.8	11.1	21330	6 AR619814	Sequence

ALIGNMENTS

RESULT 1	BC015301	2962 bp	mRNA	linear	ROD 25-JUL-2005
LOCUS	BC015301				
DEFINITION	Mus musculus ATP-binding cassette, sub-family B (MDR/TAAP), member 8, mRNA (CDNA clone MGC:19206 IMAGE:4237894), complete cde.				
ACCESSION	BC015301	GI:15929758			
VERSION	BC015301.1				
KEYWORDS	MGC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Strausberg, R.L., Feingold, R.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Cabavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., Mckernan, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, G.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalek, U., Smalleg, D.B., Scherch, A., Schein, J.E., Jones, S.J., Jones, S.J., and Marra, M.A.				
CONSTRM	Mammalian Gene Collection Program Team				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 2962)				
AUTHORS	NITH MGC Project				
CONSTRM	Direct Submission				
TITLE					

JOURNAL
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNI)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mdcdpax1.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LILNI at: <http://image.llnl.gov>
Series: IRMA Plate: 25 Row: g Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 27753994.
Location/Qualifiers

FEATURES
source

1. 2962

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:19206 IMAGE:4237894"

/tissue_type="Kidney, normal, 5 month old male mouse."

/clone_id="NCI_CGAP_K1d14"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

1. 2962

/gene="Abcb8"

/db_xref="GeneID:74610"

/db_xref="MGI:1351667"

341. 2494

/gene="Abcb8"

/product="ATP-binding cassette, sub-family B (MDR/TAP),
member 8"

/protein_id="AAH15301.1"

/db_xref="GI:15929759"

/db_xref="GeneID:74610"

/db_xref="MGI:1351667"

/translation="MLVHFRGIGRGPVGRSLQSLRPTSPASRRDRLSLRL
TYAOLRVOLRAHLPRAPASHWSPAMGVGTIVPANTMHPICLIALCEARESP
PAQTPRARELRNMLKFLPHILALGAALVALGALVAVQPLIGQVETVAK
YRDHNGSVSRKSLVQLLYGQGLITGIVLSHISNAMDRKALFESL
RDLIAFPDKTKGQVLSRLTTVOGRKSKFLVISOGLRSCVIGSLVLSLSPRL
TEMLAVTALMGVITLMGSGRLSRQCOQIARATGADALGNVTRVAFAMER
EERVOALBESCCCAEELRGIALFOGLSNIAPNCMTGLFISGLVAGQOLKGD
LMSPLVASQTVORSMASLSLVFGVVRGAGAVPEWALSPIVPLRGVYCI PKDI
RGSITQNTPEYRRCRGNVTKDTLKLPSKIALYVQSGGKTTVASLIERYDP
EAGSVTLDSHDKTLNPMRQCVIGFISQEVLTATTEMIRKGLDASBERVTA
AREANAHETISFPDGVSTVGERGTISGGQKRLALAKIPLTVLILDEATSLG
DAESRNVVEALDRASAGRTVIVIAHRLSTVAASISIIYMWAGVCEAGTHERLKG
GLYSEIRQTLDAISLTTPPAKPEDPKSCSKA"

ORIGIN

Query Match 88.7%; Score 415; DB 9; Length 2962;
Best Local Similarity 91.9%; Pwd. No. 4.2e-94;
Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 2 ACTGAGCTGGCCCTTGGTGGGCACTAGTGAATGTCACATCCCTTGGCTCTGGGCGG 61
DB 740 ATTGAGCTGGCCCTTGGTGGGCACTAGTGAATGTCACATCCCTTGGCTCTGGGCGG 799
QY 62 CTGAGTGAAGATTGTGCGCAAGTACAGAGGAGCCACATGGGAGGNTGCTGTTGTAATCC 121
DB 800 CTGAGTGAAGATTGTGCGCAAGTACAGAGGAGCCACATGGGAGGNTGCTGTTGTAATCC 859
QY 122 CGAAGCTCAGCAGCCTGCTCTCTACTGACAGGATTCAGGACCTGTAAGCTTTGCA 181

DB 860 CGTAAGCTCAGCGTCCAGCTGCTCTCTACTGATGCGTGTTCAGGAGGACCTGTGCA 919
QY 182 TACCAAGTGTGCTGTGTCCACATTTGNNNGANCAATGGCCATGACATGGGAAAGCCCTT 241
DB 920 TACCAAGTGTGCTGTGTCCACATTTGNNNGANCAATGGCCATGACATGGGAAAGCCCTT 979
QY 242 TTCAGCTCCCTGCTCCGCAAGACATTCCTTTTGTGCAAAAAGACAGGAGCGT 301
DB 980 TTCAGCTCCCTGCTCCGCAAGACATTCCTTTTGTGCAAAAAGACAGGAGCGT 1038
QY 302 AGTGAAGTCTGCTGACTACTGATGATGCAAGAAATTCAGGACATCTTAACTGTGATTTN 361
DB 1039 AGTGAAGTCTGCTGACTACTGATGATGCAAGAAATTCAGGACATCTTAACTGTGATTTN 1098
QY 362 CCAGGACATGAGCAGCTGACCTGACCTGATGATGATGATGATGATGATGATGATGATG 421
DB 1099 CCAGGACATGAGCAGCTGACCTGACCTGATGATGATGATGATGATGATGATGATGATG 1158
QY 422 CCTGCGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
DB 1159 CCTGCGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205

RESULT 2
BC085781
LOCUS
DEFINITION
Rattus norvegicus ATP-binding cassette, sub-family B (MDR/TAP),
member 8 (predicted), mRNA (cDNA clone MGC:93731 IMAGE:7107433),
complete cds.

ACCESSION
BC085781
VERSION
KEYWORDS
SOURCE

ORGANISM
Rattus norvegicus (Norway rat)

REFERENCE
AUTHORS
Straube, R.L., Feingold, R.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Dietzen, L., Maruina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Udell, T.B., Toshitsuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abrahamson, R.D., Mulle, S.J., Bosak, S.A., McSwain, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Hellton, E., Kettelman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, R.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalka, U., Smalins, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Mammalian Gene Collection Program Team
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2851)

JOURNAL
PUBMED
REFERENCE
AUTHORS
CONSRM
TITLE
CONSRM
TITLE
JOURNAL
REMARK
COMMENT
NIH MGC Project
Direct Submission
Submitted (01-NOV-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNI)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-hgc.stanford.edu>
Contact: (Dickson, Mark) mcdoxaki.stanford.edu
Dickson, M., Schmitz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/INL ac: <http://image.llnl.gov>
Series: IRAC Plate: 181 Row: f Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 56119151.

FEATURES

source

1. 2851

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="MGC:93731 IMAGE:7107433"

/issue_type="Kidney, rat (Brown Norway)"

/clone_1b="N1H MGC_235"

/lab_host="DH10B"

/note="Vector: pExpress1"

1. 2851

/gene="Abcb8_predicted"

/note="synonym: Abcb8"

/db_xref="GeneID:362302"

/db_xref="RGD:1307655"

44. 2188

/gene="Abcb8_predicted"

/codon_start=1

/product="ATP-binding cassette, sub-family B (MDR/TAP), member 8 (predicted)"

/protein_id="AA85781.1"

/db_xref="GI:55715994"

/db_xref="GeneID:362302"

/db_xref="RGD:1307655"

/translation="MLVLRVGIKGGPVPRMSLQSLRQTSAAASSDDPSSCLLR

AVAOQLSQAHLPRSPAPSHRSTSAMCWGTLVPAVMOPRCLALCAKSP

PAQTPARELRFKMLFPHLPHLALALALALALALALALALALALALALAL

YREHYGSPVSSRLSLOLLLYGQGLTFGLVLSHMGSRMMDRKAFLSLL

RODIAPPAKTRQQLYSRLTVQERSSPKYISQISSTQVIGSLMTLSLRL

ETMLAVTPALMGVTLMSGLKLSRQCCQJAPARTVADELGSVRYTAPAMKR

EBERYQAEIESCCCKABEELRGIALFGVGSINAFNCMVATLFTGSLVAGQDKGD

LMSPFVATVQVSMASLSTFGVAVGSLAGARVBYMSLSPVLTGYS1PSKDL

RGSLITQVNSFSPCRPGFVNLKPLPGKVALVQSGGKXTVALSLERFYPD

TACVVTLDGHDATLDPSPMLRGVIGISGEPVLPATTMENIRFGLDSDSEVTA

ARKANAHERFISFPDGYSTVYGERGTLSSGGQRLAIAIALKRPVLTIDATSL

DASERIVQELDRASAGRTVLVAHRLSTVRAHSLITVANGQVCEAGTHERLQKG

GLYAEILRRQALDASLPSAPPAKRPDRHSCQ"

ORIGIN

Query Match 80.8%; Score 378.2; DB 9; Length 2851;
Best Local Similarity 86.9%; Pred. No. 8.4e-85;
Matches 406; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

2 ACTGAGCTGCGCTTGGTGGCGCACTAGTGAATGTGCAATCCCTTCTCTGGGCGAG 61

443 ATTGTGCTGGCCTTGGTGGCGCACTAGTGAATGTGCAATCCCTTCTCTGGGCGCA 502

62 CTGGTGAAGATTGTGGCAAGTACAGAGGAGCAATGGGAGAGTCTGTTGANTCC 121

503 CTGGTGAAGATTGTGGCAAGTACAGAGGAGCAATGGGAGAGTCTGTTGANTCC 562

122 CGNAGGCTGCGCTTGGTGGCGCACTAGTGAATGTGCAATCCCTTCTCTGGGCGAG 181

563 CGTAGGCTGCGCTTGGTGGCGCACTAGTGAATGTGCAATCCCTTCTCTGGGCGAG 622

182 TACCTAGTGTCTGTCCCACTTANNANCMATGGCCATGNAATGCGAAAGCCCTT 241

623 TACCTAGTGTCTGTCCCACTTANNANCMATGGCCATGNAATGCGAAAGCCCTT 682

242 TTGAGTCTCTGTCTGGCGAAGATGCTTTTGTATGCAAAAAGACGGGACAGCT 301

Db 683 TTGAGTCTCTGTCTGGCGAAGATGCTTTTGTATGCAAAAAGACGGGACAGC-T 741

Qy 302 ACTGAGTGTCTGACTACTGATGTGCAAGATTTGAAGGATCCCTTGAAGCTGTCAATMN 361

Db 742 AGTAGGCGCTTGAAGTGTGCAAGATTTGAAGGATCCCTTGAAGCTGTCAATMN 801

Qy 362 CGAGGATGCGCTTGAAGTGTGCAAGATTTGAAGGATCCCTTGAAGCTGTCAATMN 421

Db 802 CGAGGATGCGCTTGAAGTGTGCAAGATTTGAAGGATCCCTTGAAGCTGTCAATMN 861

Qy 422 CCTGCGCTTGAAGTGTGCAAGATTTGAAGGATCCCTTGAAGCTGTCAATMN 468

Db 862 CCTGCGCTTGAAGTGTGCAAGATTTGAAGGATCCCTTGAAGCTGTCAATMN 908

RESULT 3
AK222911
LOCUS
DEFINITION
Homo sapiens mRNA for ATP-binding cassette, sub-family B, member 8 variant, clone: HRC04144.
ACCESSION
AK222911
VERSION
AK222911.1 GI:62897380
KEYWORDS
FLI CDNA; oligo capping.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
Oligo-capping: a simple method to replace the cap structure of eukaryotic mRNAs with oligoribonucleotides
JOURNAL
PUBMED
Gene 138 (1-2), 171-174 (1994)
8125298
AUTHORS
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
TITLE
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library
JOURNAL
PUBMED
Gene 200 (1-2), 149-156 (1997)
9373149
AUTHORS
Suzuki, Y., Sugano, S., Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A. and Yokoyama, S.
TITLE
Direct Substitution
JOURNAL
PUBMED
Submitted (22-Apr-2005) Akiko Tanaka, RIKEN Yokohama Institute, Protein Research Group; 1-7-22 Suehiro, Tsurumi, Yokohama, Kanagawa, 230-0045, Japan (E-mail: aktanaka@riken.jp, <http://protein.gsc.riken.jp/>, Tel:81-45-503-9452, Fax:81-45-503-9450)
URL: <http://www.k.u-tokyo.ac.jp/index.html.en>.
URL: <http://www.k.u-tokyo.ac.jp/index.html.en>.

COMMENT

This work was supported in part by the National Project on Protein Structural and Functional Analysis, Ministry of Education, Culture, Sports, Science and Technology of Japan.
Sumio Sugano, Yutaka Suzuki
Laboratory of Functional Genomics Department of Medical Genome Sciences Graduate School of Frontier Sciences The University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639 Japan email: sugano@k.u-tokyo.ac.jp
URL: <http://www.k.u-tokyo.ac.jp/index.html.en>.

FEATURES

source

1. 2308

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HRC04144"

/cell_type="Primary human renal epithelial cells"

/issue_type="Kidney"

/clone_1b="HRC"

/note="Cloning vector: pMR18PFL3
this clone is also named as hss001001883"

<67. .2223
/note="Start codon is not identified."
/codon_start=1

CDS


```

Yoshida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A.,
Hara,H., Tanase,T., Nomura,Y., Togiyu,S., Komai,F., Hara,R.,
Takeuchi,K., Arita,M., Imose,N., Mutsahino,K., Yuuki,H., Oshima,A.,
Sasaki,N., Aotaka,S., Yoshikawa,Y., Matsumura,H., Ichihara,T.,
Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S.,
Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H.,
Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Matsumoto,T.,
Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,
Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M.,
Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y.,
Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N.,
Inagaki,H., Ikema,Y., Okamoto,S., Okitani,K., Kawakami,T.,
Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,
Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T.,
Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
Nagase,T., Nomura,N., Kikuchi,H., Masubo,Y., Yamashita,R.,
Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)

TITLE
JOURNAL
PUBMED
14702039

AUTHORS
2
Ninomiya,K., Nagatsuna,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsubu,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Igono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Mateno,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Ohnishi,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahara,K., Masubo,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 2392)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team) ; 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3966)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB) ; cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.) ; 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
1..2392
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRAM2017455"
/class_type="amygdala"
/clone_id="BRAM2"
/note="Cloning vector: pMB18SFL3"
74..2179
/note="unnamed protein product"
/codon_start=1
/db_xref="GI:21753735"
/translacion="MLVLPFRVGRGPPFGRLLPPLPFPQTSFSAVRYSDVGRSSLLR
AVAHLSQIAWHLPRALLGPMVLSKPHLCVLCBAEBAPPASSTPHVGVSRNML
FMQPLPHLIVGVAIVLALGAALVWQIPLLGQVYVAKYRDHVGSPMESNL
STHLILGVQGLTFGLVLSHVGERRAVNDRBALPSSILRQDITPPNRTGQV
SRLLTVDQEFKSLVLSQGLRSCVAGCLVLSMLSTLTLVAVATPALMGVGT
LMGSLKRLSRQCOBOIARAGVADBEALGNVRYARAGREBERGABIEACRCA
BELGRLALFQGLSNIANCMVGLTFTGSLVAGQOVLGDSVTFVAVAGTQVRSA
NLSVLPQVVRGLSAGAVPEVMSLNPICIPLSGGCCPKBQLRSGSVFQVCFYPCR
PGREVLADPILTPRQKIVLVQSGGGKTVASLRFPDPTGVMLQORDLRDRTD
PSMLRGVVGFISEPLVFTTINENRFGLESDERVTYTAAREANHEPTSPSPG
YNTVGERGTTLSGQKORLAIRALIKQPIVLTLDRTSLDLSERVVOEALDRAS

```

ORIGIN

AGRTVLVIAHRLSTVGAHCTVWADGRVWEAGTBELLKKGGLYAEILRQALDAPR
 TRAPPKPKRBSRSHQHS"

Query Match 67.5%; Score 316; DB 8; Length 2392;
 Best local similarity 78.9%; Pred. No. 4,4e-69;
 Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

```

5 GAGCTGGCTTAAAGTGGCGCACTAGTGAATGTGCAAGATCCCTTGTCTCTGGCCGACG 64
428 GGTGCTGGCTTAAAGTGGCGCACTAGTGAATGTGCAAGATCCCTTGTCTCTGGCCGACG 487
65 GTGAGATTTGTGGCAAGTACAGAGGACCAAGGGGAGGAGGAGGAGGAGGAGGAGGAGG 124
488 GTAGAGGTGTGGCAAGTACAGAGGACCAAGGGGAGGAGGAGGAGGAGGAGGAGGAGG 547
125 AAGCTCAGCAGCAGCAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 184
548 AATCTCAGCAGCAGCAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 607
185 CTAGTCTCTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 244
608 CTGCTCTCTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 667
245 AGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 304
668 AGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 726
305 GAGTGCCTTGACTAGTATGTCGAAAGTTCGAAGCATCTTGAAGTTCGAAGTTCGAAGT 364
727 GAGCCCTTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
365 GGGACTGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 424
787 GGGGCTGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 846
425 TGCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 468
847 AGCCCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 890

```

COMMENT

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

CDS

RESULT 6
 LOCUS CQ717207 2417 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 3141 from Patent WO2068579.
 ACCESSION CQ717207
 VERSION CQ717207.1 GI:42278064
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Euteleostomi; Mammalia; Eutheria;
 Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
 Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
 KITS, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 Patent: WO 02068579-A 3141 06-SBP-2002;
 PB Corporation (NY) (US)
 Location/Qualifiers
 1..2417
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES

SOURCE

ORIGIN

Query Match 67.5%; Score 316; DB 6; Length 2417;
 Best local similarity 78.9%; Pred. No. 4,4e-69;
 Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;
 5 GAGCTGGCTTAAAGTGGCGCACTAGTGAATGTGCAAGATCCCTTGTCTCTGGCCGACG 64

Db 450 GTGCTGACCTTGTGGTGGGCACTGCTGTAATGTACAGATCCCTGCTCTGCGGCAAGCTG 509
QY 65 GTGGAATTTGTGCGCAAGTACACAGAGGACCAATGGGGAGTNTGNTGANTCCCGN 124
Db 510 GTAGAGGTGTGGCCAAAGTACAAAGGACCAAGTGGAGATTTCATGATCTAGTCCAG 569
QY 125 AAGCTCAGNCAGCAGTGTCTCTACTGACAGGATTCAGAGNACTGATGACCTTNGATAC 184
Db 570 AATCTCAGACCACTGCTTATCTCTATGATGTCTCAGGAGCTGTGACCTTGGGGTAC 629
QY 185 CTAGTGTCTGTCTCCCACTTGNNGANCATGGCCATGACATGCGGAAAGCCCTTTTC 244
Db 630 CTGGTGTCTGTCTCCCACTTGGCCAGGACATGCTGTGGACATCGGAGGCGCCCTCTTC 689
QY 245 AGCTCCCTGTCTCGGCAAGACATTTGCTTTTGTGATGCAAAAAGACAGGGAGGCTAGT 304
Db 690 AGCTCCCTGTCTCCGACACATCTCTCTTTGAGCCATTAAGACAGGGACG-19GT 748
QY 305 GAGTGTCTTACTGATGTGCAAGATTCAGAGCATCTTAAAGCTTGTGATNTCCA 364
Db 749 GAGCGGCTTGAACAATGACGAGGATTTAAGTATCTTCAAGCTTGTATCTCCCA 808
QY 365 GGGACTGACAGCTGACCCAGGTGATTTGTAGCTGTGAGNCCCTGNTATGCTGACCC 424
Db 809 GGGGCTGCAAGACTGACCCAGGTGAGCTGCTGTGTGCTCTGTCTCATGCTGTGAC 868
QY 425 TGCGCTTACCTGTGATGTGCTGNNNGACACCCGCGCTCATGG 468
Db 869 ACGCTCAGCGTGTGCTGATGTGTGCGCACACAGCCCTGATGG 912

RESULT 7
BD156975 2487 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD156975
VERSION BD156975.1 GI:27862733
KEYWORDS JP 2002191363-A/11818.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 2487)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof.
TITLE Patent: JP 2002191363-A 11818 09-JUL-2002;
JOURNAL HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/11818
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KOORU
PI SAITO,K
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10, C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
FEATURES
source location/Qualifiers
1. .2487
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 67.5%; Score 316; DB 6; Length 2487;
Best Local Similarity 78.9%; Pred. No. 4.4e-69;

Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;
QY 5 GAGTGTGCTTAAAGGTGGGAGCACTGTGATGTGACAGATCCCTGCTCTGCGGCAAGCTG 64
Db 523 GTGCTGCTGTGGGTGGGAGCACTGTGATGTGACAGATCCCTGCTCTGCGGCAAGCTG 582
QY 65 GTGGAATTTGTGCGCAAGTACACAGAGGACCAATGGGGAGTNTGNTGANTCCCGN 124
Db 583 GTAGAGGTGTGGCCAAAGTACAAAGGACCAAGTGGAGATTTCATGATCTAGTCCAG 642
QY 125 AAGCTCAGNCAGCAGTGTCTCTACTGACAGGATTCAGAGNACTGATGACCTTNGATAC 184
Db 643 AATCTCAGACCACTGCTTATCTCTATGATGTCTCAGGAGCTGTGACCTTGGGGTAC 702
QY 185 CTAGTGTCTGTCTCCCACTTGNNGANCATGGCCATGACATGCGGAAAGCCCTTTTC 244
Db 703 CTGGTGTCTGTCTCCCACTTGGCCAGGACATGCTGTGGACATGCGGAGGCGCCCTCTTC 762
QY 245 AGCTCCCTGTCTCGGCAAGACATTTGCTTTTGTGATGCAAAAAGACAGGGAGGCTAGT 304
Db 763 AGCTCCCTGTCTCCGACACATCTCTCTTTGAGCCATTAAGACAGGGACG-19GT 821
QY 305 GAGTGTCTTACTGATGTGCAAGATTCAGAGCATCTTAAAGCTTGTGATNTCCA 364
Db 822 GAGCGGCTTGAACAATGACGAGGATTTAAGTATCTTCAAGCTTGTATCTCCCA 881
QY 365 GGGACTGACAGCTGACCCAGGTGATTTGTAGCTGTGAGNCCCTGNTATGCTGACCC 424
Db 882 GGGGCTGCAAGACTGACCCAGGTGAGCTGCTGTGTGCTCTGTCTCATGCTGTGAC 941
QY 425 TGCGCTTACCTGTGATGTGCTGNNNGACACCCGCGCTCATGG 468
Db 942 ACGCTCAGCGTGTGCTGATGTGTGCGCACACAGCCCTGATGG 985

RESULT 8
AX878013 2487 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 12918 from Patent EP1074617.
ACCESSION AX878013
VERSION AX878013.1 GI:40032749
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and their use
TITLE Patent: EP 1074617-A 12918 07-FEB-2001;
JOURNAL Research Association for Biotechnology (JP)
FEATURES
source location/Qualifiers
1. .2487
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="unassigned protein product"
/codon_start=1
/protein_id="CAE89973.1"
/db_xref="GI:40032750"
/translation="MTVHLFRVGTIRGQFPGRLLPLRFTQFSVAVNTMRNGKTGOLH
KABEYSDGTRSSSLRAVAVHLRSLQNAHLPRALPRKSSBANCYQALGPMVLS
KHPHLCTVLCBAEAPPPASSTPHVDSRFRWKLFWPLRPHLLVLAVALAAL
VNVQIPLILQQLVAVVAYTRDHWGFWTEQNLSTHLLILYQGLTFGLYLVLS
VGERMAVDNRRLFSSILRQDITFEDANKTQLVSLTTDQEFKSPKVISQGLRS
CTOVAAGLIVLSMSTRLTLILMTATPALMGSLGSLKLRQCCOROBQIARAWGVA
DELAGNRTVAAPFAMQREBERRGALREACGCRABEIGRIALFQGLSNIAFNCMLV
TLTGTGSLVAGQQLTGSDMLFLVASTQVQSSMANLSVLPQVYTRGLSAGARVPRYA
LNPCTPLSGCCVPRKEDLRGSVTFQNVCFSPCRPGFVLDFTLLPGLKIVALVG
SGGKTTVASILIERFDYPTAGVWMDGRDLTLDPSPWLRGQVGFISQSPVLFETTM

ORIGIN

ENIRFGKLEASDEEYVTAAREANHEFTSPPEGNTVVGERTLLSGQOKRLAIAR
ALIKOPTVILIDEATSAIDABESERVQALDASAGRTVLVAHLSTVRAGACTIVM
ADGRWEAGTHBELKKGGLVYALIRQALDAPRTAAPPKBEPBRSOHKS"

Query Match 67.5%; Score 316; DB 6; Length 2487;
Best Local Similarity 78.9%; Pred. No. 4,4e-69;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

5 GAGCTGGCCCTTGGAGGCGGACATGAGTGAATGTCAGATCCCTGCTCGGCGGACGCTG 64
523 GTGCTGGGCTTGGAGGCGGACATGAGTGAATGTCAGATCCCTGCTCGGCGGACGCTG 582
65 GTGAGATTTGTCGCCAAGTACAGAGGACCAATGCGGAGATNTGNTGATCCGCG 124
583 GTAGAGGTGTGCGCCAAATGACAGAGGACCAATGCGGAGATNTGNTGATCCGCG 642
125 AAGCTCAGCAGCAGTGTCTCTCTACTGACAGAGTTCAGAGTCTGTTGATCCGTTGATC 184
643 AATCTCAGACCCACCTGCTTATCTCTATGCTCAGAGGACCTGCTGACCTTCGAGTAC 702
185 CTAGAGCTGCTGTCACCATGNNGANCATGAGGACCATGACATGCGGAAAGCCCTTTTC 244
703 CTGAGTCTGCTGTCACCATGNNGANCATGAGGACCATGACATGCGGAAAGCCCTTTTC 762
245 AGCTCCCTGCTGTCACCATGNNGANCATGAGGACCATGACATGCGGAAAGCCCTTTTC 304
763 AGCTCCCTGCTGTCACCATGNNGANCATGAGGACCATGACATGCGGAAAGCCCTTTTC 821
305 GAGTGGCTTGAATGAGTGAATGTCAGATCCCTGCTCGGCGGACGCTG 364
822 GAGCCGCTTGAATGAGTGAATGTCAGATCCCTGCTCGGCGGACGCTG 881
365 GGGACCTGACAGTGAATGTCAGATCCCTGCTCGGCGGACGCTG 424
882 GGGGCTGACAGTGAATGTCAGATCCCTGCTCGGCGGACGCTG 941
425 TGACCTTACCTGAGTGTGCTGNNGANCATGAGGACCATGACATGCGGAAAGCCCTTTTC 468
942 AGCCCTCAGCAGTGTGCTGNNGANCATGAGGACCATGACATGCGGAAAGCCCTTTTC 985

RESULT 9 2487 bp mRNA linear PRI 30-JAN-2004
AK002018 Homo sapiens cDNA FLJ11516 fis, clone PLACE1006956, weakly similar
LOCUS to ATP-DEPENDENT PERMEASE MDL1.
DEFINITION AK002018
ACCESSION AK002018
VERSION AK002018.1 GI:7023645
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakatsuki, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Ohyaishi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, T.,
Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
Tanikawa, M., Yamazaki, M., Nishimura, K., Ishihashi, T., Yamashita, H.,
Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,
Hirakawa, S., Chiba, Y., Ishida, S., Oho, Y., Takiguchi, S., Watanabe, S.,
Yosida, M., Hattori, T., Kusanagi, J., Kanehori, K., Takahashi, F.,
Hara, H., Tanase, T., Nomura, Y., Togliya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A.,
Sasaki, N., Aotsuma, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shiohata, N., Sano, S., Moriya, S., Motiyama, H., Sato, H., Takami, S.,
Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

COMMENT
JOURNAL
PUBMED
REFERENCE
AUTHORS

FEATURES

source
1..2487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1006956"
/tissue_type="Placenta"
/clone_1b="PLACB1"
/note="Cloning vector: pME18SFL3"
67..2274
/note="unnamed protein product"
/codon_start=1
/protein_id="BA092038.1"
/db_xref="GI:7023645"
/translation="MTVHLFRVINGRPPGRLPLPRTFSAVANTWRNKGTLQHL
KAEGRYSDGSRSSLLRAVAHLRQMLHPLPAPAPRSPSPAMCVGALGALPMTLS
KPHFCIVLACABEAPAPASSTPHVVGSRPMKLPFPLPLVLVGVAVLALGAL
VAVQIPLLGLQVAVVAKTRPHVSGPMTESQNTSLHLLITLVGGLLPTVYLLSH
VGERNAVDMRRALFSLRLQDTTFPDANTQGLVRLTVDVPSFSSFLVLSQGLS
CTQVAGCVLSMLSTRLLTLMVATPALMGVTLGSGRLSRQCGQIARAWGVA
DEALGNVTRAFAPMORREBERYGALECHRAELGIGIALFGLSINIRAVCVTG
TLFGLSVAGGOLGGLMSPLVASQVORAMNLSVFGVVNLGASARVAVYGA
INPCIPLSGCGCCVPEQRLRGSTVPCVSPCRGPFVTLKPTLLPGKIVAVLGG
SGGKGTVASLLERTYDTPAGVYMLDGRDLTIDBSRLAGQVYVPSIQPVPFGTITM
ENIRFGKLEASDEEYVTAAREANHEFTSPPEGNTVVGERTLLSGQOKRLAIAR
ALIKOPTVILIDEATSAIDABESERVQALDASAGRTVLVAHLSTVRAGACTIVM
ADGRWEAGTHBELKKGGLVYALIRQALDAPRTAAPPKBEPBRSOHKS"

CDS

ORIGIN

Query Match 67.5%; Score 316; DB 6; Length 2487;
Best Local Similarity 78.9%; Pred. No. 4,4e-69;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

5 GAGCTGGCCCTTGGAGGCGGACATGAGTGAATGTCAGATCCCTGCTCGGCGGACGCTG 64
523 GTGCTGGGCTTGGAGGCGGACATGAGTGAATGTCAGATCCCTGCTCGGCGGACGCTG 582

[illegible]

DB	TITLE	REFERENCE	AUTHORS	COMMENT
Db				
790	CTGATGCTGCTGTCCTCCACGTTTGGGAGCGATGGCTGTGACATGACATGGGAGGCGCTTCTTC			
Qy	245 AGCTCCCTGCTCCGGCAGACATGCTTTTMTTGTATGTCACAAAAGACAGGGCAGCTGACT			
Db	850 AGCTCCCTGCTCCGACAGACATCATCCTCTTTTGAACCCCAATTAAGACAGGGCAGC-TGGT			
Qy	305 GAGTCGCTTGAACATCTATGATGTCAGAAATTCAGAGGACCTTAAAGCTTGTCAATNTCCA			
Db	909 GAGCGGCTTGAACATCTATGATGTCAGAAATTCAGAGGACCTTAAAGCTTGTCAATNTCCA			
Qy	365 GGAACATGACAGCTGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT			
Db	969 GGGGCTGCGAAGCTGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT			
Qy	425 TCGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT			
Db	1029 ACGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT			
RESULT 11				
LOCUS				
AK128129				
DEFINITION				
AK128129				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
CDS				

REFERENCE 1 (bases 1 to 2383)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 15507 09-JUL-2002;
Helix RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/15507
PF 09-JUL-2002
PI 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SATO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
FEATURES
source Location/Qualifiers
FT CDS (524)..(2167).
1..2383
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 64.6%; Score 302.4; DB 6; Length 2383;
Best Local Similarity 78.4%; Pred. No. 1.2e-65;
Matches 364; Conservative 0; Mismatches 98; Indels 2; Gaps 2;
QY 5 GAGTGGCCTTAAAGTGGCGGCACTAGTGAATGAGATCCCTGCTGCGGCGGCAAGCTG 64
DB 420 GTGCTGGCCTTGGGAGCGGCACTCGTGAATGACAGATCCCTGCTGCGGCGGCAAGCT- 478
QY 65 GTGAGATTGTGGCCAAAGTACAGAGGACCAATGGGAGGANTGNTGNTGANTCCCGN 124
DB 479 GTAGAGGTGTGGCCAAAGTACAGAGGACCAATGGGAGGANTGNTGANTCCCGN 538
QY 125 AAGCTCAGNCANCTGCTCTTACTGACGACGAGTTCAGGACCTGTTGAGATC 184
DB 539 AATCTCAGACTCACTGCTTATCTCTATGATGATCAGGACCTGCTGAGGCTTCGGGTAC 598
QY 185 CTAGAGCTGCTGTCACCATTTGNNGANCATGGGACCATGACATGGGAAAGCCCTTTTC 244
DB 599 CTGGTGTCTGTCTCCACGTTGGCGGACCATGGCTGTGACATGGGAGGCGCTCTTC 658
QY 245 AGCTCCCTGCTCCGCGAAGACATGCTTTNTTGTATGATCCAAAAGACAGGCGGTAGT 304
DB 659 AGCTCCCTGCTCCGCGAAGACATGCTTTNTTGTATGATCCAAAAGACAGGCGGTAGT 717
QY 305 GAGTGGCTTGACTAGTATGACAGATTCAGGCACTCTTAAAGCTTGTCAATNNCA 364
DB 718 GAGCGCTTGAACAATGACAGTGTGACAGATTTAAGTATCTTCAAGCTTGTATCTCCA 777
QY 365 GGGAGCTGNCAGCTGACCCAGGTGATTGATGCTGAGNCCCTGNNATATGTCNCCC 424
DB 778 GGGAGCTGNCAGCTGACCCAGGTGATTGATGCTGAGNCCCTGNNATATGTCNCCC 837
QY 425 TGGCCTTAACTGATGCTGCTGANNNGACACCCGCTCATAGG 468
DB 838 ACGCCTCAAGCTGCTGATGATGATGACCAACAGCCCTCATAGG 881
RESULT 14
AX884014 2383 bp DNA linear PAT 17-DEC-2003
LOCUS AX884014
DEFINITION Sequence 18919 from Patent EP1074617.
ACCESSION AX884014
VERSION AX884014.1 GI:40038915
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: JP 1074617-A 18919 07-FEB-2001;
Research Association for Biotechnology (JRP)
FEATURES
source Location/Qualifiers
1..2383
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
524..2170
/note="unassigned protein product"
/codon_start=1
/protein_id="CA892200.1"
/db_xref="GI:40038916"
CDS
/translation="MTSSQNLSTHLILLYGVGILLTPGYLVLSHVGERRMAVDNRRL
PSSILRODITPPDANKGQLYSRLTTPVOEFKSSFKVLISGLASCTGVAGCLVLSM
LSTRLLIMVATTPALMGVGTLMGSGRLKRSRCCOQIARMAKGRADSLGVTYTRAP
AMEGRERERVGAELEACRCRAEISLRGIALFQGISNIAFNQMVIGTLFTGGSLVAGQO
LVTGDLMSFLVAGTQVRSMAISLVLRQVVRGASAGARVEYALNAPCIPLSGCCV
PKSOLRGSVTFQNTCFSPKPGFEVLDFLTLPKPGKIVLVQSGGAGKTVASLSE
RFYDPTAGVWMLDGRDLRTLDPSWLRGVGVFIISBPVLFRTTIMENIRPKLASDS
EYVTAARBAHNERFTSPRGNTVIVBERGTLSGGOKORAIARALIKOPTVILIDE
ATSLADLSERVVDBALDRASAGTIVYIARLSTYKRAHCIVVMADGRVBAOTHS
LTKRGQYASLIRQALDAPRTAAPPPKPGEPKSHQKS"

ORIGIN
Query Match 64.6%; Score 302.4; DB 6; Length 2383;
Best Local Similarity 78.4%; Pred. No. 1.2e-65;
Matches 364; Conservative 0; Mismatches 98; Indels 2; Gaps 2;
QY 5 GAGTGGCCTTAAAGTGGCGGCACTAGTGAATGAGATCCCTGCTGCGGCGGCAAGCTG 64
DB 420 GTGCTGGCCTTGGGAGCGGCACTCGTGAATGACAGATCCCTGCTGCGGCGGCAAGCT- 478
QY 65 GTGAGATTGTGGCCAAAGTACAGAGGACCAATGGGAGGANTGNTGNTGANTCCCGN 124
DB 479 GTAGAGGTGTGGCCAAAGTACAGAGGACCAATGGGAGGANTGNTGANTCCCGN 538
QY 125 AAGCTCAGNCANCTGCTCTTACTGACGACGAGTTCAGGACCTGTTGAGATC 184
DB 539 AATCTCAGACTCACTGCTTATCTCTATGATGATCAGGACCTGCTGAGGCTTCGGGTAC 598
QY 185 CTAGAGCTGCTGTCACCATTTGNNGANCATGGGACCATGACATGGGAAAGCCCTTTTC 244
DB 599 CTGGTGTCTGTCTCCACGTTGGCGGACCATGGCTGTGACATGGGAGGCGCTCTTC 658
QY 245 AGCTCCCTGCTCCGCGAAGACATGCTTTNTTGTATGATCCAAAAGACAGGCGGTAGT 304
DB 659 AGCTCCCTGCTCCGCGAAGACATGCTTTNTTGTATGATCCAAAAGACAGGCGGTAGT 717
QY 305 GAGTGGCTTGACTAGTATGACAGATTCAGGCACTCTTAAAGCTTGTCAATNNCA 364
DB 718 GAGCGCTTGAACAATGACAGTGTGACAGATTTAAGTATCTTCAAGCTTGTATCTCCA 777
QY 365 GGGAGCTGNCAGCTGACCCAGGTGATTGATGCTGAGNCCCTGNNATATGTCNCCC 424
DB 778 GGGAGCTGNCAGCTGACCCAGGTGATTGATGCTGAGNCCCTGNNATATGTCNCCC 837
QY 425 TGGCCTTAACTGATGCTGCTGANNNGACACCCGCTCATAGG 468
DB 838 ACGCCTCAAGCTGCTGATGATGATGACCAACAGCCCTCATAGG 881
RESULT 15
AK024401 2383 bp mRNA linear PRI 30-JAN-2004
LOCUS AK024401
DEFINITION Homo sapiens cDNA FLJ14339 f18, clone SKNMC1000013, highly similar

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 16:27:08 ; Search time 470 Seconds
(without alignments)
6636.332 Million cell updates/sec

Title: US-10-327-713-267
Perfect score: 468
Sequence: 1 gactgagctgcgccttagtgc.....ngncacacccgcctcatg 468

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	316	67.5	2392 11	ADM01573 Human CDN
2	316	67.5	2417 6	ABK34832 Human CDN
3	316	67.5	2487 4	AAH14983 Human CDN
4	316	67.5	2562 3	AAD00603 Human mem
5	316	67.5	3212 13	ACN41862 Human dia
6	316	67.5	5089 13	ADRO7889 Full leng
7	315	67.3	1211 3	AACT7613 Human ORF
8	302.4	64.6	2383 4	AAH18672 Human CDN
9	277.6	59.3	1251 3	AAA62022 Hydrophob
10	277.6	59.3	1617 3	AAA62032 Hydrophob
11	230	49.1	2317 13	ACN41861 Human dia
12	219.6	46.9	1805 6	ABL89954 Human pol
13	206.8	44.2	994 9	ACH43729 Human foe
14	206.8	44.2	1023 4	AAE22411 Human sec
15	186.2	39.8	744 4	AAH08411 Human CDN
16	127.8	27.3	423 4	AAFP92351 Bovine ma
17	117.6	25.1	425 9	ACH47047 Human inf
18	93	19.9	2379 9	ABD03511 Drosophila
19	93	19.9	4940 4	ABJ03510 Drosophila

20	88	18.8	662	4	AAH07823	AAH07823 Human CDN
21	74	15.8	283	4	AAI02575	AAI02575 Human rep
22	74	15.8	283	5	AAH40273	AAH40273 DNA encod
23	74	15.8	283	11	ADJ09268	ADJ09268 Human pro
24	55.4	11.8	574	6	ABL90156	ABL90156 Human pol
25	51.8	11.1	1647	14	ACL67748	ACL67748 M. xanthu
26	51.8	11.1	1773	13	ADT44704	ADT44704 Bacterial
27	51.8	11.1	21330	14	ACL64746	ACL64746 M. xanthu
28	46.4	9.9	560	3	ACF76564	ACF76564 Human ORF
29	46.4	9.9	1743	14	ACL67610	ACL67610 M. xanthu
30	46.4	9.9	1773	13	ADT44685	ADT44685 Bacterial
31	46.4	9.9	24602	14	ACL64739	ACL64739 M. xanthu
32	44	9.4	434	5	ABV30083	ABV30083 Human pro
33	44	9.4	483	5	ABV45555	ABV45555 Human pro
34	40.8	8.7	9104	13	ADQ39136	ADQ39136 Human SNP
35	40.8	8.7	9258	12	ADP45448	ADP45448 Human var
36	40.8	8.7	9260	12	ADQ87183	ADQ87183 Human tum
37	40.8	8.7	9260	12	ADQ84906	ADQ84906 Human tum
38	40.8	8.7	9272	8	ABX76157	ABX76157 Lung canc
39	40.8	8.7	9272	12	ADQ18965	ADQ18965 Human sof
40	40.8	8.7	9272	13	ADQ05813	ADQ05813 Novel bro
41	40.8	8.7	9272	14	ADQ05806	ADQ05806 Cyclin-de
42	40.8	8.7	9277	13	ADQ39138	ADQ39138 Human SNP
43	40.8	8.7	9287	6	ABK64501	ABK64501 Human ben
44	40.8	8.7	9456	12	ADQ23327	ADQ23327 Human sof
45	40.2	8.6	455	9	ACH12996	ACH12996 Human adu

ALIGNMENTS

RESULT 1
ADM01573
ID ADM01573 standard; cDNA; 2392 BP.

XX ADM01573;

DT 20-MAY-2004 (first entry)

DE Human cDNA of the invention SEQ ID NO:258.

KW seq; gene; human; gene therapy; diagnostic marker; pharmaceutical.

OS Homo sapiens.

PN EPI347046-A1.

PD 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S, Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I, Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;

XX WPI; 2003-723558/69.

XX P-PSDB; ADM04016.

XX New polynucleotides and polypeptides are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.

XX Claim 1, SEQ ID NO 258; 305bp; English.

XX The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

PI Hillman JL, Yue H, Tang YT, Lal P, Corley NC, Guegler KJ;
 PI Baughn MR, Azimzai Y, Lu DM;
 DR WPI: 2000-365576/31.
 DR P-PSDB: AAY71059.
 PT Novel human membrane transport proteins useful for diagnosis, prevention
 PT and treatment of membrane transport disorders, immune/inflammatory
 PT disorders and cell proliferative disorders including cancer.

Claim 9, Page 113-114, 136pp; English.

XX The present sequence is a cDNA encoding membrane transport protein, MTRP-
 CC 4 from Incyte clone 2274290 isolated from human PROSNO1 cDNA library.
 CC MTRP-4 shows homology to human ATP-binding cassette (ABC) transporter (GI
 CC 4321407) and Schistosoma mansoni ABC family protein, SMDR1. It is
 CC expressed in reproductive, nervous, gastrointestinal and
 CC hematopoietic/immune tissues. The present sequence is useful in
 CC diagnosis, prevention and treatment of disorder related with increased
 CC or decreased expression of MTRP such as familial goitre, Menkes disease,
 CC diabetes, Parkinson's disease, neurological disorders such as Alzheimer's
 CC disease, depression, epilepsy, schizophrenia, immune/inflammatory
 CC disorders such as AIDS, Addison's disease, allergies, atherosclerosis,
 CC Graves disease, gout, Hashimoto's thyroiditis, viral, bacterial, fungal,
 CC parasitic, protozoal or helminthic infections and cell proliferative
 CC targets in microarrays. MTRP DNA is also useful for generating
 CC hybridisation probes useful in mapping genomic sequences and detecting
 CC differences in sequences among normal, carrier and affected individuals.
 CC It is also used for screening libraries of compounds in drug screening
 CC techniques

XX Sequence 2562 BP; 444 A; 824 C; 793 G; 501 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 3; Length 2562;
 Best Local Similarity 78.9%; Pred. No. 1e-80;

Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 5 GAGCTGGGCTTAAAGTGGGCACTAGTGAATGAGATCCCTGCTCGGCGCAGCTG 64
 DB 484 GTGCTGGGCTTAAAGTGGGCACTAGTGAATGAGATCCCTGCTCGGCGCAGCTG 543
 QY 65 GTGAGATTTGTGCGCAAGTACACAGAGGACCAATGAGGAGTNTGANTCCGCGN 124
 DB 544 GTAGAGGTGTGGCCAAATGACACAGAGGACCAATGAGGAGTNTGANTCCGCGN 603
 QY 125 AAGCTTCANCGANCCTGCTCTACTGNAACGAGTTGAGNACTGAGATAC 184
 DB 604 AATCTCAGACCCACCTGCTTATCTCTATGAGTTCAGAGACTGCTGACCTTCGGGTAC 663
 QY 185 CTAGTGTCTGTCTCCCACTTGNANCGATGAGGACATGAGGAGAAACCTTTTC 244
 DB 664 CTGTGTCTGTCTCCCACTTGNANCGATGAGGACATGAGGAGAAACCTTTTC 723
 QY 245 AAGTCCCTGCTCGGCAAGATGTTGTTNTTGAATGCAAAAAGACAGGAGAGT 304
 DB 724 AGCTCCCTGCTCGGCAAGATGTTGTTNTTGAATGCAAAAAGACAGGAGAGT 782
 QY 305 GAGTGTCTGACTACTGATGTGCAAGATTCAGAGGATCTTAAAGCTTGTCAATMCCA 364
 DB 783 GAGCGGCTTGACAACTGACGTGACAGAGTTTAAATGATCCTTCAAGCTTGTATCTCCA 842
 QY 365 GGGATCTGACAGTGAACCAAGTATGTTAGTACCTGAGAGCCCTGANTATGTCGCC 424
 DB 843 GGGGCTGACCAAGTGAACCAAGTATGTTAGTACCTGAGAGCCCTGANTATGTCGCC 902
 QY 425 TGACCTTACCTGATGCTGAGCTGANNNGACAACCGGCGCTCATGG 468
 DB 903 AGGCTTCAAGCTGCTGCTATGATGTGACCAACCAAGCTCATGG 946

RESULT 5
 ACN41862

ID ACN41862 standard; cDNA; 3212 BP.
 XX ACN41862;
 XX ACN41862;
 DT 18-NOV-2004 (first entry)
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:737.
 XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
 KW dthp.
 XX Homo sapiens.
 OS
 XX MO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 XX
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthorne TR, Suchorolski MT, Altus CM, Pltts SJ, Elder IV;
 PI Mooney BM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens K, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin BH;
 PI Perella CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Scuve LI;
 PI Lesage RB, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kirtson BS;
 PI Xu Y, Kwong M, Policky JI, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patuxy S, Shi X, Suarez CJ;
 XX
 DR WPI: 2004-329368/30.
 DR P-PSDB: ABM83210.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.

PS Claim 1, Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2122 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorders, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dthp polynucleotide of
 CC the invention. Note: The sequence data for this patent is not represented
 CC in the printed specification, but was obtained in electronic format
 CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 3212 BP; 565 A; 1056 C; 938 G; 653 T; 0 U; 0 Other;

Query Match 67.5%; Score 316; DB 13; Length 3212;
 Best Local Similarity 78.9%; Pred. No. 1.1e-80;

Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 5 GAGCTGGGCTTAAAGTGGGCACTAGTGAATGAGATCCCTGCTCGGCGCAGCTG 64
 DB 538 GTGCTGGGCTTAAAGTGGGCACTAGTGAATGAGATCCCTGCTCGGCGCAGCTG 597
 QY 65 GTGAGATTTGTGCGCAAGTACACAGAGGACCAATGAGGAGTNTGANTCCGCGN 124
 DB 598 GTAGAGGTGTGGCCAAATGACACAGAGGACCAATGAGGAGTNTGANTCCGCGN 657

KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KM	bone damage; cartilage damage; antiinflammatory disease; coagulation;
KM	thrombosis; contraceptive; ss.
XX	
OS	Homo sapiens.
XX	
PN	MO200058473-A2.
XX	
PD	05-OCT-2000.
XX	
PF	31-MAR-2000; 2000WO-US008621.
XX	
PR	31-MAR-1999; 99US-0127607P.
PR	02-APR-1999; 99US-0127636P.
PR	05-APR-1999; 99US-0127728P.
PR	30-MAR-2000; 2000US-00540763.
XX	
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shinketsu RA, Leach M;
XX	
DR	WPI; 2000-602362/57.
DR	P-PsDB; AAB42404.
XX	
XX	
PT	Novel nucleic acids and peptides derived from open reading frame X,
PT	useful for treating e.g. cancers, proliferative disorders,
PT	neurodegenerative disorders and cardiovascular disease.
XX	
PS	Claim 5; Page 3530-3531; 5507pp; English.

CC AAC74446 to AAC77606 encode the proteins given in ABA02037 to ABA33387,
CC which represent the human ORF open reading frames 1 to 361. The ORF
CC sequences have activities such as: cytostatic; hepatotropic; vulerary;
CC antiproliferic; antiparasinian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antirheumatic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antihyproid; and antianemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORF-associated disorder. The nucleic acids can be used to express ORF
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
CC
XX Sequence, 1211 BP; 228 A; 372 C; 358 G; 253 T; 0 U; 0 Other;

QY	246	GCTCCCTCTCCGGGAACATTCCTTTTGTGAGCCAAAAAGAAAGGCGAGCGTAGTG	305
Db	359	GCTCCCTCTCCGAAGAAGCATCACCCTCTTTTGAGCCCATATAGAACAGGGAGAC-TGGTG	417
QY	306	AGTCCTTGACTACTGATGTGCAAGAAATTCAAGGATCCCTTNAAGCTTGTCAATTCCAG	365
Db	418	AACCGCTTGAACAATGACTGACAGAGATTAAATATCTTTCAAGCTTGTCAATCTCCAG	477
QY	366	GGACTGAGCACTGNAACCCAGGTGATTGGTAGCCTTGAGNCCCTGNNATATGCTGNCCTT	425
Db	478	GGGCTGCAAAAGCTGACCCAGAGTGACAGGCTGCTGTGTTCCCTGTCCATGCTGTGACA	537
QY	426	CGCCTTACCTTGATGTGTGGCTGNNANCAACCCGCCCTCATGG	468
Db	538	CGCCTCAAGCTGTCTGTATGTGTGGCAACACAGGCCCTATGG	580

```

RESULT8
AAH18672
ID   AAH18672 standard; cDNA, 2383 BP.
XX
XX
XX   AAH18672;
AC
XX
XX   26-JUN-2001 (first entry)
DT
DE   Human cDNA sequence SEQ ID NO:18919

```

OS Homo sapiens.
XX
XX
PN EP1074617-A2.
XX
XX
XX 07-FEB-2001.
XX
XX
PF 28-JUL-2000; 2000BP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX
PA (HELI-) HELIX RES INST.
PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX
DR WPI; 2001-318749/34.
XX
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
XX cDNAs.
XX
PS Claim 8; SEQ ID NO 18919; 2537pp + Sequence Listing; English.
XX
XX
CC The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by

Db 180 GGTGAGCCGCTGACACAGTGCAGAGATTAAATCATCTTCAAGCTGTATCTC 239
QY 362 CAGAGGACCTGACAGTGCAGAGTGTATGAGCCCTGAGGAGCCCTGATATCTGAC 421
Db 240 CAGAGGAGCTGACAGTGCAGAGTGTATGAGCCCTGAGGAGCCCTGATATCTGAC 299
QY 422 CCTGAGCCCTTACCTGATGCTGAGTGTATGAGCCCTGAGGAGCCCTGATATCTGAC 468
Db 300 GACAGGCTTCAAGCTGTATGAGTGTGAGCCACACAGGCTTCAAGTATG 346
RESULT 13
ACH43729
ID ACH43729 standard; cDNA, 494 BP.
XX ACH43729;
AC ACH43729;
XX 13-OCT-2003 (first entry)
DT 13-OCT-2003 (first entry)
XX Human foetal brain cDNA #4454.
DS Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
KM Homo sapiens.
XX US2003073623-A1.
PN 17-APR-2003.
XX 30-JUL-2001; 2001US-00918995.
PF 30-JUL-2001; 2001US-00918995.
XX 30-JUL-2001; 2001US-00918995.
PR 30-JUL-2001; 2001US-00918995.
XX (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONR/) JONES L W.
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX MPI; 2003-615964/58.
DR New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridisation probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX Claim 1, SEQ ID NO 30941; 44pp; English.
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX obtained in electronic format directly from UNIPROT at
XX segdata.uniprot.org/sequence.html?docID=20030073623
SQ Sequence 494 BP; 84 A; 158 C; 135 G; 108 T; 0 U; 9 Other;

Query Match 44.2%; Score 206.8; DB 9; Length 494;

Best Local Similarity 80.1%; Pred. No. 2e-49;
Matches 229; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 5 GAGCTGGCTTAAAGTGGGCGGCACTAGTGAATGTGAGATCCCTGCTCTGGGCGCAGCTG 64
Db 208 GTGCTGGCTTAAAGTGGGCGGCACTAGTGAATGTGAGATCCCTGCTCTGGGCGCAGCTG 267
QY 65 GTGAGATTTGTGCGCAATAGACAGAGGACCAATGGAGAGTNTGNTGTAATCCCGAN 124
Db 268 GTAGAGGTGCTGCGCAATAGACAGAGGACCAATGGAGAGTNTGNTGTAATCCCGAN 327
QY 125 AAGCTGAGTGTGCGCAATAGACAGAGGACCAATGGAGAGTNTGNTGTAATCCCGAN 184
Db 328 AATCTCAGACACCACTGCTTATCTTATGATGTCAGAGGACCTGCTGCGGATAC 387
QY 185 CTAGTGTGCTGCTGCGCAATAGACAGAGGACCAATGGAGAGTNTGNTGTAATCCCGAN 244
Db 368 CTGCTGCTGCTGCTGCGCAATAGACAGAGGACCAATGGAGAGTNTGNTGTAATCCCGAN 447
QY 245 AGCTCCCTGCTCTGCGCAATAGACAGAGGACCAATGGAGAGTNTGNTGTAATCCCGAN 290
Db 448 AGCTCCCTGCTCTGCGCAATAGACAGAGGACCAATGGAGAGTNTGNTGTAATCCCGAN 493
RESULT 14
AAF22411
ID AAF22411 standard; cDNA, 1023 BP.
XX AAF22411;
AC AAF22411;
XX 26-MAR-2001 (first entry)
DT 26-MAR-2001 (first entry)
XX Human secreted protein gene 39 SEQ ID NO:49.
DE Human secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic;
XX cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
XX fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
XX rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
XX cardiovascular disorder; cerebrovascular disorder; cerebral ischemia;
XX angiogenesis; nervous system disorder; Alzheimer's disease; infection;
XX ocular disorder; corneal infection; wound healing; skin aging;
XX food additive; preservative; ss.
OS Homo sapiens.
XX WO20061629-A1.
PN 19-OCT-2000.
XX 06-APR-2000; 2000WO-US009071.
PF 09-APR-1999; 99US-0128694P.
XX 20-JAN-2000; 2000US-0176931P.
PR (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX Ruben SM, Komatsoulis G;
PI MPI; 2000-647420/62.
DR P-PSDB; AAB63172.
XX Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.
XX Claim 1; Page 450-451; 533pp; English.
XX AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134
XX to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
XX and polypeptides homologous to them. Human secreted proteins have
XX activities based on the tissues and cells the genes are expressed in.
XX Examples of activities include: immunosuppressive; antiarthritic;

THIS PAGE BLANK (USP10)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:56:09 ; Search time 3081 Seconds
(without alignments)
7106.899 Million cell updates/sec

Title: US-10-327-713-267

Perfect score: 468
Sequence: 1 gactgagctgacctgagctg.....ngmcacaccgcctcatcg 468

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	436	93.2	468 10	CG663507 OST448795
2	415	88.7	751 6	CR249142 UT-M-FCO-
3	415	88.7	1659 4	AK014688 Mus muscu
4	415	88.7	2154 10	AY407420 Mus muscu
5	415	88.7	2647 4	AK049152 Mus muscu
6	415	88.7	2669 4	AK038760 Mus muscu
7	415	88.7	2676 4	AK014319 Mus muscu
8	415	88.7	2779 4	AK030624 Mus muscu
9	414	88.5	780 6	CA945430 UT-M-FD0-
10	411.8	88.0	2699 4	AK076315 Mus muscu
11	400.2	85.5	553 8	CK211935 MNS16502
12	392.8	83.9	771 2	B1147958 602912678
13	329.2	70.3	750 6	CP726195 UT-M-GZ0-
14	321.2	68.6	628 3	BT738314 603361553
15	317.6	67.9	4340 4	CR857093 Pongo Pyg
16	316	67.5	572 3	BQ189757 UT-R-E01-
17	316	67.5	625 3	BM783111 K-BEST0060
18	316	67.5	674 3	BM930206 UT-R-E01-
19	316	67.5	1484 4	CR599833 full-leng
20	316	67.5	1553 4	CR610778 full-leng
21	316	67.5	1553 4	CR616094 full-leng
22	316	67.5	1594 4	CR592221 full-leng

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
CG663507	OST448795	Mus musculus 129SV/Bv Mus musculus cDNA clone OST448795,	CG663507	CG663507.1	GI:37487356	GSS.	Mus musculus (house mouse)	Zambrowicz, B.P., Abuln, A., Ramirez-Solis, R., Richter, L.J., Figgott, J., Beltrandi, R., Buxton, E.C., Edwards, J., Finch, R.A., Fiddie, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaring, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.	
		Mus kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention						Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)	
		14610273							
		Contact: Zambrowicz BP							
		OmniBank							
		Lexicon Genetics Incorporated							
		4000 Research Forest Drive, The Woodlands, TX 77381, USA							
		Email: materials@lexgen.com							
		Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)							
		Class: Gene trap.							
		Location/Qualifiers							
		1. 468							
		/organism="Mus musculus"							
		/mol_type="mRNA"							
		/strain="129SV/Bv"							
		/db_xref="taxon:10090"							
		/clone="OST448795"							
		/cell_type="embryonic stem cell"							
		/clone_id="Mus musculus 129SV/Bv"							

ALIGNMENTS

Query Match	Score	DB ID	Length
93.2%	436	10	468

Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GACATGAGCTGGGCTTATGAGGCGGCACTGATGTAATGCAATCCCTGCTCCGCGGCA 60
Db 1 GACTAGGCTGGGCTTATGAGGCGGCACTGATGTAATGCAATCCCTGCTCCGCGGCA 60
QY 61 GCTGTGAGATGTTGCGCAAGTACACGAGGACCACTGGGAGATGTCGTTGATGATC 120
Db 61 GCTGTGAGATGTTGCGCAAGTACACGAGGACCACTGGGAGATGTCGTTGATGATC 120
QY 121 CCGNAAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 180
Db 121 CCGNAAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 180
QY 181 AATACCTAGTGTGCTGTCCCAATGNNCAGATGCGCATGNAATGCGGAAAGCCCT 240
Db 181 AATACCTAGTGTGCTGTCCCAATGNNCAGATGCGCATGNAATGCGGAAAGCCCT 240
QY 241 TTTCAAGCTCCCTGCTCCGCGGCAAGACATGCTTTTGTGATGCGCAAAAGACAGGCGAG 300
Db 241 TTTCAAGCTCCCTGCTCCGCGGCAAGACATGCTTTTGTGATGCGCAAAAGACAGGCGAG 300
QY 301 TAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 TAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 NCCAGGAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
Db 361 NCCAGGAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
QY 421 CCCCTGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
Db 421 CCCCTGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
```

RESULT 2
LOCUS CB249142 751 bp mRNA linear EST 15-JUL-2003
DEFINITION UI-M-PCO-bym-c-23-0-UI.r1 NIH_BMAP_PCO Mus musculus cDNA clone
IMAGE:5720014 5', mRNA sequence.
ACCESSION CB249142
VERSION CB249142.1 GI:2838256
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurigmachi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 751)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
[found through the I.M.A.G.E. Consortium/LLNL](http://image.llnl.gov), at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: PYX-5.

FEATURES
source Location/Qualifiers

```
1..751
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5720014"
/tissue_type="whole brain"
```

/dev stage="embryo 12.5 dpc"
/lab host="DH10B (T1 phage resistant)"
/clone lib="NIH BMAP_PCO"
/notes:Organ: brain; Vector: PYX-Asc; Site 1: BcoR I;
Site 2: Not I. The library was constructed according to
Bonaldo, Lemon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction.
ligated with BcoR I adaptor, digested with Not I, and then
cloned directionally into PYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is TGAGAGAGCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). "Gene Discovery in the Developing Mouse Nervous
System", supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

Query Match 88.7%; Score 415; DB 6; Length 751;
Best Local Similarity 91.9%; Pred. No. 2.3e-107;
Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

```
QY 2 ACTGAGCTGGGCTTATGAGGCGGCACTGATGTAATGCAATCCCTGCTCCGCGGCGAG 61
Db 109 ATTGAGCTGGGCTTATGAGGCGGCACTGATGTAATGCAATCCCTGCTCCGCGGCGAG 168
QY 62 CTGTGTGAGATGTTGCGCAAGTACACGAGGACCACTGGGAGATGTCGTTGATGATC 121
Db 169 CTGTGTGAGATGTTGCGCAAGTACACGAGGACCACTGGGAGATGTCGTTGATGATC 228
QY 122 CCGNAAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 181
Db 229 CCGNAAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 288
QY 241 TTTCAAGCTCCCTGCTCCGCGGCAAGACATGCTTTTGTGATGCGCAAAAGACAGGCGAG 300
Db 241 TTTCAAGCTCCCTGCTCCGCGGCAAGACATGCTTTTGTGATGCGCAAAAGACAGGCGAG 360
QY 301 TAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 TAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 361 NCCAGGAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
Db 361 NCCAGGAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
QY 421 CCCCTGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
Db 421 CCCCTGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 528
```

RESULT 3
LOCUS AK014688 1659 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
library, clone:4833412N02 product:ATP-binding cassette, sub-family
B (MDR/TPA), member 8, full insert sequence.
ACCESSION AK014688
VERSION AK014688.1 GI:12852691
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurigmachi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Identification and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE

AUTHORS 3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Komno H., Akiyama,J., Nishi,K., Kitsuami,T., Tashtiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,O.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE

AUTHORS 4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE

AUTHORS 5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE

AUTHORS 6 (Bases 1 to 1659)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arawaka,T., Bono,H., Carninci,P., Fukuda,S., Fukuichi,Y.,
Furuno,M., Hangaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
Hiracka,T., Hoti,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
Kasubawa,T., Kato,H., Kawai,J., Kojima,Y., Komno,H., Kouda,M.,
Koya,S., Kuwahara,C., Macpyma,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ono,M., Okazaki,Y., Okido,T., Owa,C.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D.,
Shibata,K., Shiba,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toyota,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Yumatsesu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physiological and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGACGATCCAGACCTCTTTTCTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 10.0 and subtraction to
Rot = 100.0. Second strand cDNA was prepared with the primer
adapter of sequence [5'
GAGAGAGACGATTCGATTAAATTAATATTCCTCCCCCCC 3']. cDNA was cleaved
with BamHI and XhoI. cDNA of size compressed longer than 7 kb was
selected before cloning. Vector: a modified pBlueScript KS(+) after
bulk excision from lambda PLC I. Cloning sites, 5' end: SalI, 3'
end: BamHI. Host: DH10B.
Location/Qualifiers

source

1. 1659

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="PANTOM DB:483412N02"

/db_xref="taxon:10090"

/clone="483412N02"

/issue_type="head"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="0 day neonate"

1. 1659

/note="ATP-binding cassette, sub-family B (MDR/TMP), member 8 (MD)|MDI:1351667, GB|A213191, evidence: BLASTN, 99%, match=370"

misc_feature

Query Match 88.7%; Score 415; DB 4; Length 1659;

Best Local Similarity 91.9%; Pred. No. 2,8e-107;

Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

ORIGIN

Query 2 ACTGAGCTGGCCCTTAAGTGTGGGCACTAGTGAATGTGAGATCCCTTGCTCTGGGCGAG 61

Ds 493 ATTGTGCTGGCCCTTAAGTGTGGGCACTAGTGAATGTGAGATCCCTTGCTCTGGGCGAG 552

Qy 62 CTGGTGGAGATTGTGCGCAAGTACACAGAGGAGCCACATGGGGAGTTCGTGTGATGCC 121

Ds 553 CTGGTGGAGATTGTGCGCAAGTACACAGAGGAGCCACATGGGGAGTTCGTGTGATGCC 612

Qy 122 CGNAGCTCAGCAGCCAGCTGCTCTTACTGACAGTTCAGGACTGATGACCTTNGGA 181

Ds 613 CGTAACTCAGCGCTCAGCTGCTCTTACTGATGACGATGTCAGGGAGCTGATCTTGGGA 672

Qy 182 TACTTAAGTGTCTGTCTCCACATTGANNANCAATGGCCATGACATGGCGGAAAGCCCTT 241

Ds 673 TACCTAAGTGTCTGTCTCCACATTGANNANCAATGGCCATGACATGGCGGAAAGCCCTT 732

Qy 242 TTGAGCTCCCGCTGCTGGGCAAGACATGCTTTTATGATGCAAAAAGACAGGCGACGT 301

Ds 733 TTGAGCTCCCGCTGCTGGGCAAGACATGCTTTTATGATGCAAAAAGACAGGCGAC-T 791

Qy 302 AGTAGTGTGCTTGAAGTACTGATGTGCAAGATTCAGAGCATCTTNAAGCTTGTGATNTN 361

Ds 792 AGTAGTGTGCTTGAAGTACTGATGTGCAAGATTCAGAGCATCTTNAAGCTTGTGATNTN 851

Qy 362 CCAGGAGCTGNGACAGCTGAAACCAAGTGTGTTGTTAGCTTGAAGNCCCTGANNATAGCTGNC 421

Ds 852 CCAGGAGCTGNGACAGCTGAAACCAAGTGTGTTGTTAGCTTGAAGNCCCTGANNATAGCTGNC 911

Qy 422 CCTCTGCTTACCTGATGCTGCTGATGAGGATGAGGAGCCGAGCTGATGAG 468

Ds 912 CCTCTGCTTACCTGATGCTGCTGATGAGGATGAGGAGCCGAGCTGATGAG 958

RESULT 4

LOCUS AY407420 2154 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus ABCB8 gene, VIRUAL TRANSCRIPT, partial sequence,

ACCESSION AY407420

KEYWORDS genomic survey sequence.

VERSION AY407420.1 GI:39763391

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Mus.

1 (bases 1 to 2154)

Clark,A.G., Glatowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sultsky,J.J., Adams,M.D. and Cargill,M.

Interfering nonneutral evolution from human-chimp-mouse orthologous gene clones

REFERENCE	TITLE	COMMENT	FEATURES	ORIGIN
JOURNAL PUBMED 14671302	Science 302 (5652), 1960-1963 (2003)			
AUTHORS	2 (bases 1 to 2154)			
	Clark,K.A.G., Gianhowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
	Submitted (16-Nov-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
	This sequence was made by sequencing genomic exons and ordering them based on alignment.			
	Location/Qualifiers			
	1..2154			
	/organism="Mus musculus"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:10090"			
	<1..>2154			
	/gene="ABC8"			
	/locus_tag="HCM2884"			
	Query Match	88.7%; Score 415; DB 10; Length 2154;		
	Best Local Similarity	91.9%; Pred. No.3e-107;		
	Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1			
Dy	2 ACTGAGCTGGCCCTTAGTGTGGGCACTAGTAATGTGCAGATCCCTTGCTCTGGCCGAC	61		
Db	400 ATTGTGCTGGCCCTTAGTGTGGGCACTAGTAATGTGCAGATCCCTTGCTCTGGCCGAC	459		
Dy	62 CTGGTGGAGATTGTGCCAAGTACGAGGAGCCACATGGGGAGMTCATGTTAATCC	121		
Db	460 CTGGTGGAGATTGTGCCAAGTACGAGGAGCCACATGGGGAGTTCATGTCTGATGCC	519		
Dy	122 CGNAAGCTCAGCAGCAGCAGCTGCTCTACTGAGACAGATTCAGAGACTGTGACTTTGGA	181		
Db	520 CGTAAAGCTCAGCAGCTGCTGCTCTACTGAGACAGATTCAGAGACTGTGACTTTGGA	579		
Dy	182 TACCTAGTGTGTGTGTCCCACTTGNANNCATGGCCATGACATGCGAGAAACCTT	241		
Db	580 TACCTAGTGTGTGTGTCCCACTTGNANNCATGGCCATGACATGCGAGAAACCTT	639		
Dy	242 TTGAGCTCCCTGTGCTGGGCAAGACATTTGCTTTTGTGATGCCAAAGACAGGCGAGCT	301		
Db	640 TTGAGCTCCCTGTGCTGGGCAAGACATTTGCTTTTGTGATGCCAAAGACAGGCGAGCT	698		
Dy	302 AGTGAAGCTGCTTGAATCTAGTATGTSCAAGAAATTCAAGGCACTCTTAAGCTTGATNTN	361		
Db	699 AGTGAAGCTGCTTGAATCTAGTATGTSCAAGAAATTCAAGTATCTCTTCAAGCTTGATNTN	758		
Dy	362 CCAAGGACTGAGCAGCTGAGCCCAAGATGATTTGTGAGCTGAGAGCCCTGATNTATCTGNC	421		
Db	759 CCAAGGACTGAGCAGCTGAGCCCAAGATGATTTGTGAGCTGAGAGCCCTGATNTATCTGNC	818		
Dy	422 CCTTGCTTGAATCTGATGTGTGCTGAGGAGCAACCCGCTGATG	468		
Db	819 CCTTGCTTGAATCTGATGTGTGCTGAGGAGCAACCCGCTGATG	865		
RESULT 5				
LOCUS	AK049152			
DEFINITION	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone: C330007P20 product: Atp-binding cassette, sub-family B (MDR/TP), member 8, full insert sequence.			
ACCESSION	AK049152.1			
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCES
AUTHORS

- 1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
- 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
- 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Saeki, N., Carninci, P.,
Konno, H., Akiyama, U., Nishi, K., Kitenaka, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, J.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kite, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
- 4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
- The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2647)
- Adechi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Ohsato, N.,
Okazaki, Y., Salto, R., Satoh, H., Sakai, C., Sakai, R., Sakazume, N.,
Sano, H., Saeki, D., Shibata, K., Shimagawa, F., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
- Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC)
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
- cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
1 . 2647
/organism= "Mus musculus"
/mol_type= "mRNA"
/strain= "C57BL/6J"
/db_xref= "FANTOM DB:C330007P20"
/db_xref= "taxon:10090"
/clone= "C330007P20"
/cell_type= "ES cells"

FEATURES
SOURCE

CDS

/clone_11b="RIKEN full-length mouse cDNA library"
85..2238
/note="unnamed protein product; ATP-binding cassette,
sub-family B (MDR/TAP), member 8 (MD1/MG1.1351667,
GblAP213391, evidence: BLASTN, 99%, match=370)
putative"
/codon_start=1
/protein_id="BAC33571.1"
/db_xref="GI:26339816"
translation="MLVHFRGIRGAPVGNLSLRPOTSEARSDDRLSHLLR
TVAOLRVOLRAH.PRA.PASHMSPSAMCVGLVAVPVMOPRLCLALCEAKXP
PQAPTRAPELREKWKLPFRPHHIALALALVLAAGALVNOIPLIGOLVETAK
YRDHWGSPVSESRKLSVOLLNIGVGLITGVLVSHIGERNAMDRKALFSL
RODIAPFDAAKQGVLRLLTVQVSEKSPKVI SQGLSCVQVLSLSLSERL
TLMLAVTALMGVTLMSGLSKLSRQCEQIARATGVADBLGNVTRVAFAMER
BEERYOALESCCKKABELRGIALFOGLSNIFNCMVGLTFPGSLVAGQCKGD
LMSPLVASQTVOSMRSVTLFGVVRGISAGARVEMALSVIPLTGYCIPNDI
RGSITQNTFTSPKPRGVNLDPTLKPSGKIVLNQSGGKTTVASLIERFDP
EAGSVTLDDHDLKTNPSWLRGVIFGISEPVLPATTTNIRRKLDASDEVTYA
AREANAHFISPPDGYSTVYGERGTLTSGQQLALNALIKQPLVILDEATSL
DAEERVQBALDRASGRVIVIAHRLSTVRAHSIIYMANQVCEAGTHBELKKG
GLYSELIRQGTLDASLTSPPAKPDPKSCQSKA"

ORIGIN

Query Match 88.7%; Score 415; DB 4; Length 2647;
Best local Similarity 91.9%; Pred. No. 3.1e-107;
Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 2 ACTGAGCTGGCTTGGTGGGCACTAGTGAATGTGCAGATCCCTGCTCCCTGGCCAG 61
DB 484 ATTGTGCTGGCTTGAAGTGGGCACTAGTGAATGTGCAGATCCCTGCTCCCTGGCCAG 543
QY 62 CTGGTGAAGATTGGCCAGATGACAGAGGAGCACTAGGAGAGTTCCTGCTGAGTCC 121
DB 544 CTGGTGAAGATTGGCCAGATGACAGAGGAGCACTAGGAGAGTTCCTGCTGAGTCC 603
QY 122 CGNAAAGCTCAGCAGCAGCTGCTCTTACTGACAGAGTTCAGNAGTGTGATCTTNGA 181
DB 604 CGTAAAGCTCAGCAGCTGCTCTTACTGACAGAGTTCAGNAGTGTGATCTTNGA 663
QY 182 TACCTAGTCTGCTGCTCCACATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 241
DB 664 TACCTAGTCTGCTGCTCCACATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
QY 242 TTGAGCTCCCTGCTCGGAGAGACATTTGTTTATGTCAGAAAGAGAGGAGGAGGAG 301
DB 724 TTGAGCTCCCTGCTCGGAGAGACATTTGTTTATGTCAGAAAGAGAGGAGGAGGAG 782
QY 302 AGTGAAGTGGCTTGACTAGTATGTGCAAGATTCAAGGAGCTCTTNAAGCTTGCATNTN 361
DB 783 AGTGAAGTGGCTTGACTAGTATGTGCAAGATTCAAGGAGCTCTTNAAGCTTGCATNTN 842
QY 362 CCAGAGACTGAGAGCTGAGACCCAGGAGTATTTGAGCTGAGAGCCCTGANTATGCTGNC 421
DB 843 CCAGAGACTGAGAGCTGAGACCCAGGAGTATTTGAGCTGAGAGCCCTGANTATGCTGNC 902
QY 422 CCCCTGGCTTACCTGAGTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468
DB 903 CCCCTGGCTTACCTGAGTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 949

RESULT 6

AK038760

LOCUS

DEFINITION

AK038760 2669 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male hypothalamus cDNA, RIKEN full-length
enriched library, clone:A230060K10 Product:ATP-binding cassette,
sub-family B (MDR/TAP), member 8, full insert sequence.

ACCESSION

AK038760

VERSION

AK038760.1 GI:26086722

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Carninci, P. and Hayashizaki, Y.

TITLE

High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

JOURNAL

10349636

PUBMED

11042155

REFERENCE

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

11042155

PUBMED

11042155

REFERENCE

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Huzumi, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsui, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

11076861

PUBMED

11076861

REFERENCE

4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL

11076861

PUBMED

11076861

REFERENCE

5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL

11076861

PUBMED

11076861

REFERENCE

6 (bases 1 to 2669)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Onno, M., Ohnato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

JOURNAL

11076861

PUBMED

11076861

REFERENCE

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

JOURNAL

11076861

PUBMED

11076861

REFERENCE

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

JOURNAL

11076861

PUBMED

11076861

REFERENCE

URL: http://genome.gsc.riken.jp/
URL: http://genome.gsc.riken.jp/
Location/Qualifiers

FEATURES

1..2669

SOURCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

REFERENCE

1..2669

	misc_feature	/clone="A330060K10"	/sex="male"	/tissue_type="hypothalamus"	/clone_lib="RIKEN full-length enriched mouse cDNA library"	/dev_stage="adult"	68..2222	/note="ATP-binding cassette, sub-family B (MDR/TAP), member 8 [MGI:MGI:1351667, GB AF213391, evidence: BLASTN, 99%, match=370]	
	polyA_signal	putative"	2650..2655	/note=".2655					
	polyA_site	note="putative"	2659	/note="putative"					
ORIGIN									
Query Match	88.7%; Score 415; DB 4; Length 2669;								
Best Local Similarity	91.9%; Pred. No.3.1e-107;								
Matches 429; Conservative	0; Mismatches 37; Indels 1; Gaps 1								
Dy	2 ACTGAGCTGGCGCTTGTGAGTCGCGCACTAGTAATGTGCAGATCCCTTGCTCCTGGGCCAG	61							
Dd	467 ATTGCTGCGCTTAGTGCGGCACATTAGTAATGTGCAGATCCCTTGCTCCTGGGCCAG	526							
Dy	62 CTGTGTGAAGATTGTGCGCAAGTACAAGAGGACCATGTGGAGAGTNCYTGNTGANTCC	121							
Dd	527 CTGTGTGAAGATTGTGCGCAAGTACAAGAGGACCATGTGGAGAGTTCGTGTCTGAGTCC	586							
Dy	122 CGNAAGCTCANAGNCANCTGTCTCTACTGNAONAGTTACAGNACTGNVAGACTTNGA	181							
Dd	587 CGTAGCTCAGCTCAGCTGTCTCTACTGTAAGAGTGTCAAGAGACTGTGACTTTGTA	646							
Dy	182 TACCTAGTGTCTGTCTGCCACATTTGNMGANCATGTGCATGACATGACGGAAGCCCTT	241							
Dd	647 TACCTAGTGTCTGTCTGCCACATTTGTAAGAGTGTGTGAGGACATGACATGACGGAAGCCCTT	706							
Dy	242 TTCACTCTCCCTGTCTCCGCAAGACATTTGTTTTTATGTCAAAAGAAGAGGAGCGT	301							
Dd	707 TTCAGCTCCCTGTCTCCGCAAGACATTTGTTTTTATGTCAAAAGAAGAGGAGCGC-T	765							
Dy	302 AGTAGTGTCTGTCTGACTGATGTGTGCAGAAATTCAGAGCATCTTMAAGCTGTCAATMN	361							
Dd	766 AGTAGTGTCTGTCTGACTGATGTGTGCAGAAATTCAGAGCATCTTCAAGCTTTGTATCTC	825							
Dy	362 CCAGGACTGTGACAGCTGACCCAGAGTATTTGTAGCTGTGAGNCCCTGMNTATCTGNC	421							
Dd	826 CCAGGACTGTGACAGCTGACCCAGAGTATTTGTAGCTGTGAGNCCCTGMNTATCTGNC	885							
Dy	422 CCTGTGCTTACCCTGATGTCTGTGCTGNNGNCAACCCGCGCTTCATAGG	468							
Dd	886 CCTGTGCTTACCCTGATGTCTGTGCTGNNGNCAACCCGCGCTTCATAGG	932							
RESULT 7									
LOCUS AK014319	2676 bp mRNA linear HTC 03-APR-2004								
DEFINITION Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3222401P09 product:ATP-binding cassette, sub-family B (MDR/TAP), member 8, full insert sequence.									
ACCESSION AK014319									
VERSION AK014319.1 GI:12852089									
KEYWORDS HTC; CAP trapper.									
SOURCE Mus musculus (house mouse)									
ORGANISM Mus musculus									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
REFERENCE Carninci,P. and Hayashizaki,Y.									
TITLE High-efficiency full-length cDNA cloning									
JOURNAL Meth. Enzymol. 303, 19-44 (1999)									
PUBMED 10349636									
REFERENCES									
2									

AUTHORS	TITLE	JOURNAL	PUBMED REFERENCE
Garcini,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	11042159
Shibata,K., Itoh,M., Aizawa,K., Nagaoke,S., Sasaki,N., Carinci,P., Komno,H., Ariyama,J., Nishi,K., Kitanai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,S., Matsuno,H., Sakaguchi,S., Ikegami,T., Kashiwa,K., Fujikake,S., Inoue,K., Togaw,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsumura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.	Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	Genome Res. 10 (11), 1757-1771 (2000)	11076861
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.	Functional annotation of a full-length mouse cDNA collection	Nature 409, 685-690 (2001)	
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Nature 420, 563-573 (2002)	
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arawaka,T., Bono,H., Carinci,P., Fukuda,S., Fukuishi,Y., Furumoto,M., Hanagaki,T., Hara,A., Hayastu,N., Hiramoto,K., Hirakawa,T., Horii,F., Imocani,K., Ishii,Y., Itoh.M., Izawa,M., Kanukawa,T., Kato,K., Kawasaki,Y., Kojiwa,Y., Konno.H., Koude,M., Koye,S., Kuhihara,C., Matsuyama,T., Miyazaki,A., Nishi.K., Nomura,K., Numazaki,R., Onno,M., Okazaki,Y., Okido,T., Owa.C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D., Shibata,K., Shihabe,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tegawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya.T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, url:http://genome.gsc.riken.jp/, Tel.:81-45-503-9222, Fax:81-45-503-9216)		
Please visit our web site (http://genome.gsc.riken.jp/) for further details.	CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGAAGATCCAAAGACCTCTTTTATTATTTATYVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGAATTCGAATTATTAATTAATCAATCCCCCCC 3']. cDNA was cleaved with XhoI and SacI. Cloning sites, 5' end: XhoI, 3' end: SacI.	Location/Qualifiers 1. .2676 organism="Mus musculus" mol_type="mRNA" strain="C57BL/6J" /db_xref="PANTOM_DB:3222401P09" /id_xref="taxon:10090" /clone="3222401P09" /issue type="head"	

CDS

/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="14, 17 days embryo"
72..2225
/note="unnamed protein product; ATP-binding cassette,
sub-family B (MDR/TAP), member 8 [MGI:1351667,
GB|AF213391, evidence: BLASTN, 99%, match=370]
putative"
/codon_start=1
/protein_id="BAB29270.1"
/db_xref="GI:12852090"
/translation="MKVHLFRGIRGCPVPGMSLOSIRPOTSAARSSDRLSHLR
TVAQLKVLRAHLPRAIPASMSPPAMCVGTLVPAVIMGPRCLIALCBKASP
PAQTPAPBLRPMKLFMRHLPALALGAALVAVQIPLLGLQVETVAK
YRDHMGSEVSESRKLSVOLLVYQGLITGVYLLSHIGRMAWDRKLFSSLL
RODIAFDPAKGTQVLSRLTTPVQEFKSLVIGQLSCVQISLVLSMSPRL
TLMIAVTPPALMGVTLMSGRKLSROCOIARAVADALGNVTVAPAMKR
BSRYOAEIASCCEKABEGRIALFQGLSNIAFNOMVGTPIGSLVAVAGQOLKGD
LMSPLVASQTVQSMASLSVLFGQVVRGSLAGARFVMAISLVPITGTCIPNKDI
RGSITPQNTVSPYCPKPGFNVKDFTLKLPSEKIVLVQSGGKTTVASLIERFD
ARASVTLDEHDLATLNPMLRGQVIGFISQEPVLFTTMENTIRPKLPASDEVYTA
AREANHEFTISPPDGYSTVYGERGTLISGGQRLAIALIKOPTVILDEATLAL
DAESRVQEAIDRASGRVIVIAHRLSTVRAHSLIYVANGQVCEAGTHIELKKG
GUYSELIRKQITDASLITSPPAKPRDPKSCSKA"
2653..2658
/note="putative"
2676
/note="putative"
/note="putative"

ORIGIN

Query Match 88.7%; Score 415; DB 4; Length 2676;
Best Local Similarity 91.9%; Pred. No. 3.1e-107;
Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 2 ACTGAGCTGGCCTTAGGTGGGCACTAGTGAATGTGAGATCCCTTGTCTCTGGGCGAG 61
DB 471 ATTGTGCTGGCCTTAGGTGGGCACTAGTGAATGTGAGATCCCTTGTCTCTGGGCGAG 530
QY 62 CTGGTGGAGATTTGCGCCAAAGTACACAGAGGACCACTGGGGAGTNTCNTGTGTGATCC 121
DB 531 CTGGTGGAGATTTGCGCCAAAGTACACAGAGGACCACTGGGGAGTNTCNTGTGTGATCC 590
QY 122 CGNAAAGCTCAGCCAGCTGCTCTCTAATGACGAGTTCAGGACTGATGACTTNGCA 181
DB 591 CGTAAAGCTCAGCCAGCTGCTCTCTAATGACGAGTTCAGGACTGATGACTTNGCA 650
QY 182 TACCTAGTGTGCTGTGCCCATTTGANNANCNATGGCCATGNAATGGGAAAGCCCTT 241
DB 651 TACCTAGTGTGCTGTGCCCATTTGANNANCNATGGCCATGNAATGGGAAAGCCCTT 710
QY 242 TTGAGCTCCCTGCTCGGGCAAGACATTTCTTTTATGATGCCAATAAGACAGGCGACGT 301
DB 711 TTGAGCTCCCTGCTCGGGCAAGACATTTCTTTTATGATGCCAATAAGACAGGCGACGT 769
QY 302 AGTAGAGTGGCTTGAATGATGCAAGATTTCAAGGCAATCTTNAAGCTTGTCAATNT 361
DB 770 AGTAGAGTGGCTTGAATGATGCAAGATTTCAAGGCAATCTTNAAGCTTGTCAATNT 829
QY 362 CCAGAGGACTGAGCAGCTGNAACCCAGGATTTGTGAGCCTGAGAGCCCTGANTATGCTGNC 421
DB 830 CCAGAGGACTGAGCAGCTGNAACCCAGGATTTGTGAGCCTGAGAGCCCTGANTATGCTGNC 889
QY 422 CCCTCGGCTTACCTGATGTGCTGCTGNNGCACACCGCCCTCATGG 468
DB 890 CCCTCGGCTTACCTGATGTGCTGCTGNNGCACACCGCCCTCATGG 936

RESULT 8
AK030624 2779 bp mRNA linear HTC 03-APR-2004
LOCUS AK030624
DEFINITION Mus musculus adult male pituitary gland cDNA, RIKEN full-length
enriched library, clone:5330439A07 product:ATP-binding cassette,
sub-family B (MDR/TAP), member 8, full insert sequence.
ACCESSION AK030624

VERSION
KEYWORDS
SOURCE
ORGANISM

AK030624.1 GI:26326616
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

REFERENCE
AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunari, T., Taahito, H., Itoh, M.,
Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

JOURNAL
PUBMED
REFERENCE
AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
PUBMED
REFERENCE
AUTHORS

5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
PUBMED
REFERENCE
AUTHORS

6 (bases 1 to 2779)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gscl.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

TITLE
JOURNAL

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

COMMENT

1..2779

FEATURES
SOURCE

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:5330439A07"
/db_xref="taxon:10090"
/clone="5330439A07"
/sex="male"
/tissue_type="pituitary gland"
/clone_lib="Riken full-length enriched mouse cDNA library"
/dev_stage="adult"
88..2221
/note="unnamed protein product; ATP-binding cassette,
sub-family B (MDR/TAP), member 8 (MGD) [MG1:1351667,
GB|AF213391, evidence: BLASTN, 99%, match=370]
putative"
/codon_start=1
/protein_id="BAC27052.1"
/db_xref="GI:26326617"
/translation="MLVHLFRGIRGVPVMSLQSLRFRQFSARSSDDLRLSHILR
TVAOLRVOLRAHLPRAPPSHMSPSAMCMVGTVVPAVLMOHPLCLIALCEAKESP
PAQPTRAPEIRFNMGLFWHFLPHLALGAATVLAALYVQIPLLGQVETVAK
YTRDMGSPVSESRKLSVOLLLVYQGLTFTGYVLISHGERMAMDRKALPSSLL
KODIAFPDAKTKGOLVSLRTDVQFKSPFLVISOGRSCQVIGSLVLSMLSPRL
TLMLAVTPALMGVGLMGSGIKLSROCEQIARATVADBALGNVTVSAFAMEKR
EERVOAELESCECCABELRGIALFOGLSNIAFNCVLTGTLFIGSLVAGQOLKGD
LMSPLVASQTVORSMASLSVLEQVVRGLSAGARVEXMALSPVLELGVGICIPKID
RGSITFOVNTPEYPCRPENVLKDFTLKLPSEKVALYVQSGGKTTASLSLERYTP
EAGSVTLGSHDLRTNLPSPNRQVIGFISQSEVLPAFTTMENTIRGKUDASDERVTA
AREANAHFISFPDGYSTVGEVGERGTTLSGGOKRLAIARALIIPQTVLILDEAVSL
DAESERVVOEALDRAAGRTVLIARLSVTAAHSIIVMANGVCEAGTHBELKKG
GLYSELIRROQTDAISLTSTPPEKDEPDPSQSKA"
2757..2762
/note="putative"
2779
/note="putative"

```

```

polyA_signal
polyA_site
ORIGIN

```

Query Match 88.7%; Score 415; DB 4; Length 2779;

Best Local Similarity 91.6%; Pred. No. 3.2e-107; Matches 429; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

```

2 ACTGAGCTGGCCTTAGTGGTGGGCACTAGTGAATGTGCAGATCCCTTCTCTGGGCGCAG 61
467 ATTGTGCTGGCCTTAGTGGTGGGCACTAGTGAATGTGCAGATCCCTTCTCTGGGCGCAG 526
62 CTGTGTGAGATTGTGGCAAGTACACAGAGGACACATGGGAGANTNCTGTTGANTCC 121
527 CTGTGTGAGATTGTGGCAAGTACACAGAGGACACATGGGAGATTCTGTCTGAGTCC 586
122 CGNAGCTGAGCAGCAGCTGCTCTACTGACGACGAGTTGAGGACGAGTGAAGTCTTNGA 181
587 CGTAACTGAGCAGCAGCTGCTCTACTGACGAGTTGAGGACGAGTGAAGTCTTNGA 646
182 TACCTAGTGTCTGTCTGCCAATTGNNAGNCATGGCCATGACATGGCGAAGCCCTT 241
647 TACCTAGTGTCTGTCTGCCAATTGNNAGNCATGGCCATGACATGGCGAAGCCCTT 706
242 TTGAGCTCTGTCTGTCTGCCAATTGNNAGNCATGGCCATGACATGGCGAAGCCCTT 301
707 TTGAGCTCTGTCTGTCTGCCAATTGNNAGNCATGGCCATGACATGGCGAAGCCCTT 765
302 AGTGAAGTGTCTGTCTGTCTGCCAATTGNNAGNCATGGCCATGACATGGCGAAGCCCTT 361
766 AGTGAAGTGTCTGTCTGTCTGCCAATTGNNAGNCATGGCCATGACATGGCGAAGCCCTT 825
362 CCAGGAGCTGAGCAGCTGACAGTGAATGGTGTAGCTGAGAGCCCTGNNATATGCTGAC 421
826 CCAGGAGCTGAGCAGCTGACAGTGAATGGTGTAGCTGAGAGCCCTGNNATATGCTGAC 885
422 CCCTGAGCTTACCTGATGCTGTGCTGAGGAGCAGCCGCTTCATGG 468
886 CCCTGAGCTTACCTGATGCTGTGCTGAGGAGCAGCCGCTTCATGG 932

```

```

RESULT 9
LOCUS CA945430 780 bp mRNA linear EST 09-JUL-2003
DEFINITION U1-M-PD0-cdh-p-24-0-UI r1 NIH-BMAP_PD0 Mus musculus cDNA clone
IMAGE:6829033 5', mRNA sequence.
ACCESSION CA945430
VERSION CA945430.1 GI:27433910
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsdbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMWL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyX-5.

```

FEATURES

source

```

1..780
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6829033"
/tissue_type="whole brain"
/dev_stages="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH-BMAP_PD0"
/note="Organ: brain; Vector: pyX-Asc; Site 1: Scov I,
Site 2: Not I; The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with Scov I adaptor, digested with Not I, and then
cloned directionally into pyX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is TAGAGAGCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

```

ORIGIN

Query Match 88.5%; Score 414; DB 6; Length 780;

Best Local Similarity 91.6%; Pred. No. 4.5e-107; Matches 428; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

```

2 ACTGAGCTGGCCTTAGTGGTGGGCACTAGTGAATGTGCAGATCCCTTCTCTGGGCGCAG 61
180 ATTGTGCTGGCCTTAGTGGTGGGCACTAGTGAATGTGCAGATCCCTTCTCTGGGCGCAG 239
62 CTGTGTGAGATTGTGGCAAGTACACAGAGGACACATGGGAGANTNCTGTTGANTCC 121
240 CTGTGTGAGATTGTGGCAAGTACACAGAGGACACATGGGAGATTCTGTCTGAGTCC 299
122 CGNAGCTGAGCAGCAGCTGCTCTACTGACGACGAGTTGAGGACGAGTGAAGTCTTNGA 181
300 CGTAACTGAGCAGCAGCTGCTCTACTGACGAGTTGAGGACGAGTGAAGTCTTNGA 359

```

QY 182 TACCTAGTCTGCTGTCCCACTTNGNANCATGCGCATGNAACATGGGAAAGCCCTT 241
HAYASHIDA,K., Hayatsu,M., Hiramoto,K., Hirose,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koyama,S., Kurahara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Nunakata,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akanita,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toyota,T., Yasunishi,A.,
Muramatsu,M., and Hayashizaki,Y.
Direct Submission
Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suhei-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-research@riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://phantom.gsc.riken.jp/
URL: http://location.qualifera
FEATURES
source
1..2699
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOL DB:4732414M12"
/db_xref="taxon:10090"
/clone_id="4732414M12"
/issue_type="ekin"
/clone_lib="RIKEN full-length enriched mouse CDNA library"
/dev_stage="10 days neonate"
92..2245
/note="unnamed protein product; ATP-binding cassette,
sub-family B (MDR/MDR), member 8 (MDR8) [MGI:1351667,
GDB:1213391, evidence: BLASTN, 99%, match=370]
putative"
/codon_start=1
/protein_id="BAC6297.1"
/translation="MLVHFRFGIRGPGVPMGLQSLRFPFSARSSDRLSSHLIR
TVNQLVQVLRRAHLPAPASHSBPMACWGLVAVVAVVMOHPRCLILALCRKSP
PQPTAPRLPRWKLPHRPHHLALALCAATVLAALVAVVQVLLGLVEMVAK
YRDRHNGSVFSESRKLSVOLLVGVQGLTFGLVTLVLSHGERMADRKALPSSIL
RDLIAFLDAKQQLVSRITTVQERKSPKLVISGLSCVIVISGLVLSMLSPRL
TLMLAVTALMVGTLVMSGLKLSRQCEQJARTAGVADBLAGNRTVRAAMERK
BEERYALSSCCSKABELGRLALFQGLSNLAPNCGVLTGLIGSLVGOOLKGGD
LMEFLVASQVDSMSASLSTLPGVIRGASAGARVEVMALSVIPLTGYCIPNKDI
KGSITQNTVTFSPCRPGPVLDPTLTKPSGIVLAVGSGGKTTVALIRFYP
EASVTLVDGDLTLTPSWLRGVVIGTISQVQVRLAIALIKQPLVLTDEKSTML
ARANAHFISPPDGVSTVGGRTLSGGQVQRLAIALIKQPLVLTDEKSTML
DASEVVEQALDRASGRVLAIRLHSTVRAHSTIVANQVCEAGTHBELKKG
GLVSELIROTTLASLSTPAPKPDPSQSKA"
2675..2680
polyA_signal
2699
/note="putative"
polyA_site
2699
/note="putative"
ORIGIN
Query Match 88.0%; Score 411.8; DB 4; Length 2699;
Best Local Similarity 91.4%; Pred. No. 2.6e-106;
Matches 427; Conservative 0; Mismatches 39; Indels 1; Gaps 1;
QY 2 ACTGAGCTGGCCTTAGTGGCGGCACTGATGATGTCAGATCCCTTGTCTCTGGGCGAG 61
DB 491 ATTGTGCTGGCCTTAGTGGCGGCACTGATGATGTCAGATCCCTTGTCTCTGGGCGAG 550

RESULT 10
AK076315 2699 bp mRNA linear HTC 03-APR-2004
LOCUS
DEFINITION
Mus musculus 10 days neonate skin CDNA, RIKEN full-length enriched
library, clone:4732414M12 product:ATP-binding cassette, sub-family
B (MDR/MDR), member 8, full insert sequence.
AK076315
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
2
Carninci,P., and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,T., Nishi,K., Kikunishi,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujisawa,S., Inoue,K., Togawa,K., Izawa,M., Ohara,E., Watabiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A., and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multiplexillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2699)
Adachi,J., Aizawa,K., Akiyama,T., Arakawa,T., Bono,H., Carninci,P.,

QY	62	CTGGGAGAGATTGTGTGGCCAAAGTACACGAGGAGACACATAGGGGAGATNCAATGNTGANTGCC	121
Db	551	CTGGTGGAGATGTGTGTCGCCAAGTACACGAGGAGACACATAGGGGAGATTTGCTGTCTGAGTCC	610
QY	122	CGMAAGCTCAGACGNCANCTGCTCTCTACTGMAACGAGTTCAAGMACTGNTGACCTTTGGG	181
Db	611	CGTAAGCTCAAGGCTCAAGCTGTCTCTTACTGTACGAGTGTTCAAGGACTGTGACCTTTGGG	670
QY	182	TACCTAAGTGTCTGTCTGTCCACATTGNNGANCATGGCCATGMACTGGGAAAAGCCCTT	241
Db	671	TACCTAAGTGTCTGTCTGTCCACATTGTGTAGCCACATGGCCATGTGACATYGGGAAAAGCCCTT	730
QY	242	TTCAAGCTCCGTGCTCCGGCAAGACATGTGCTTTNTTGTATGGCCAAAAGACAGGGGACGCT	301
Db	731	TTCAAGCTCCGTGCTCCGGCAAGACATGTGCTTTCTTGAATGCCAAAAGACAGGGGACGCT	789
QY	302	AGTGAAGTGGCTTGACTACTGATGTGCAAGAAATTCAAGGCATCTTAAAGCTTGATCAATNTN	361
Db	790	AGTGAAGTGGCTTGACTACTGATGTGCAAGAAATTCAAGGCATCTTAAAGCTTGATCAATCTC	849
QY	362	CCAGGAACTGAGCACTGNAACCCAGGTGATTGTGTAGCTGTGAAGNCCCTGANTATATGCTGAC	421
Db	850	CCAGGAACTGAGCACTGNAACCCAGGTGATTGTGTAGCTGTGTGCTCTGTATATGCTGTTC	909
QY	422	CCCTGAGCTTAACTCCGTAATGTGTGGCTGANNNCACACCCGGCCCTCATATG	468
Db	910	CCCTGAGCTTAACTCCGTAATGTGTGGCTGTGTATACACCCGGCCCTCATATG	956

RESULT 11				
LOCUS	CX211935	553 bp	mRNA	linear
DEFINITION	MNS16502 Mouse Neurosphere Normalized cDNA library Mus musculus			
	CDNA 5', mRNA sequence.			

ACCESSION	CX211935
VERSION	CX211935.1
KEYWORDS	GI:56867227
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 553)	Williams, C., Wirta, V., Lundberg, J., and Pilsen, J.	Expressed sequence tags of cDNA clones from murine neurospheres	Unpublished (2005)	
	Contact: Williams, C.			

Molecular Biotechnology
Institution of Biotechnology
Albanova University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel.: +4605378332
Fax: +4605378481
Email: cecilia.williams@biotech.kth.se
Seq primer: M13RW.

FEATURES	Location/Qualifiers
source	1. .553

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="MALE"
/tissue_type="lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
/dev_stage="Adult"

```

```

/clone_id="mouse neurosphere normalized cDNA library"
/ncbi="Organ: Adult brain; Vector: pCMVSPORT6.0; A cDNA
library was constructed in pCMVSPORT6.0 from RNA isolated
from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/Reagen"

```

Query Match

85.5%; Score 400.2; DB 8; Length 553;

Best Local Similarity 92.0%; Pred. No. 3.6e-103;
Matches 413; Conservative 0; Mismatches 35; Indels 1; Gaps 1.

Oy	20	GGGGCACTAGTGAATGTGCAATCCCTGTGCTCGGGCAGAGTGTGAAATTGTCCG	79
Db	1	GGGGCACTAGTGAATGTGCAATGCCCTTGTGCTCGGGCAGAGTGTGAAATTGTCCG	60
Oy	80	AAGTACAGAGGGAGCCACATGGGGAGNTNCTGTNTGANTCCCGAAGCTCAGNCCAN	139
Db	61	AAGTACAGAGGGAGCCACATGGGGAGTTCGTGTCTGATGCCCGTAACCTCAGCCCTCAG	120
Oy	140	CTGCTCTTACTAGNACAGAGTTCAAGGNACTGATGACCTTNGATACCTAGTGTGCTGTCC	199
Db	121	CTGCTCTTACTAGTGAAGTGTTCAGGGAGCTGCTGACCTTTGGATCTTAGTGTGCTGTCC	180
Oy	200	CACATTGNNGNACNATGGCCATGNACATGCGGAAAGCCCTTTTCAGCTCCCTGTCTCCGG	259
Db	181	CACATTGGTGAAGCCATGGCCATGGACATGCGGAAAGCCCTTTTCAGCTCCCTGTCTCCGG	240
Oy	260	CAAGACATTTGCTTNTTGTATGCGCAAAAGACAGGGCAGCGATGAGATGCTGTACAC	319
Db	241	CAAGACATTTGCTTCTTGTATGCGCAAAAGACAGGGCAGCG-ATGATGATGCGTTTACAC	299
Oy	320	TGATGTGCAAGAAATTCAGAGCATCCTTAAAGCTTGTCAATTNCCAGGACCTGAGAGCTG	379
Db	300	TGATGTGCAAGAAATTCAGATCATCTCTTCAAGCTTGTATCTCCAGGGACCTGCGAGCTG	359
Oy	380	NAACCAAGTGAATTGGTAGCCTGAGAGNCCCTGANTTATGCTGACCCCTCGCTTACCTGAT	439
Db	360	CACCAAGGTGAATTGGTAGCCTGAGTGTCCCTGTCTATGCTGTCTCCCTCGCTTACCTGAT	419
Oy	440	GCTGCGTNNGNACACCCGAGCCCTCATGG	468
Db	420	GCTGCGTGTGTACACCCGAGCCCTCATGG	448

RESULT	12
B147958	
LOCUS	B147958
DEFINITION	771 bp mRNA linear EST 05-JUL-2001
	60291267881 NCI-CGAP L19 Mus musculus cDNA clone IMAGE:5053602 5'
	mRNA sequence.

ACCESSION	BI147958	GI:146079555
VERSION	BI147958.1	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	Buaya'ota, Metazoa; Chondrata; Ctenulata; Vertebrata; Insecta; Mammalia; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae, Mus.	1 (bases 1 to 771)		
	NH-MGC	http://mgc.ncl.nih.gov/		
	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)		
	Contact: Robert Strusberg, Ph.D.			

Email: csapbs-remail.nih.gov
 Tissue Procurement: Jeffrey R. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM1145 row: 1 column: 19
 High quality sequence stop: 738.
 Location/Qualifiers
 1
 738

```

source
1.771
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5051602"
/lab_host="DH10B (TI phage-resistant)"
/clone_nib="NCI_CGAP_l19"

```

ORIGIN

/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

Query Match 83.9%; Score 392.8; DB 2; Length 771;
Best Local Similarity 91.1%; Pred. No. 5.1e-101;
Matches 419; Conservative 0; Mismatches 39; Indels 2; Gaps 2;

QY 2 ACTGACCTGGCCTTAGTGTGGGCACTAGGAAAGTGGAGATGCCCTTGGCTCGGGCCAG 61
DB 197 ATTGTCTGGCCTTAGTGTGGGCACTAGGAAAGTGGAGATGCCCTTGGCTCGGGCCAG 256
QY 62 CTGGTGAAGATTTGCGGCAAGTACACGAGGAGCAACATGGGAGANTTCNTGTGATCC 121
DB 257 CTGGTGAAG-TCCTCCCAAGTACACGAGGAGCAACATGGGAGANTTCNTGTGATCC 315
QY 122 CGNAGCTCAGCAGCCAGTCTCTCTA CTGACGAGTTCAGGACTGATGACCTTNGA 181
DB 316 CGNAGCTCAGCAGCTCTCTCTA CTGACGAGTTCAGGACTGATGACCTTNGA 375
QY 182 TACCTAGTGTCTCTCTCTCTA CTGACGAGTTCAGGACTGATGACCTTNGA 241
DB 376 TACCTAGTGTCTCTCTCTCTA CTGACGAGTTCAGGACTGATGACCTTNGA 435
QY 242 TTGAGCTCCCTGCTCGGCAAGACATTCCTTTTGTATGTCGCAAGAGAGAGAGCT 301
DB 436 TTGAGCTCCCTGCTCGGCAAGACATTCCTTTTGTATGTCGCAAGAGAGAGAGCT 494
QY 302 AGTGAAGTGTCTTGACTA CTGATGTGCAAGATTCAGAGCATCTTNAAGCTTGTGATNT 361
DB 495 AGTGAAGTGTCTTGACTA CTGATGTGCAAGATTCAGAGCATCTTNAAGCTTGTGATNT 554
QY 362 CCAAGGACTGAGCACTGACACCAAGTGTGTTGTTAGCTGAGACCTGATGATGTC 421
DB 555 CCAAGGACTGAGCACTGACACCAAGTGTGTTGTTAGCTGAGACCTGATGATGTC 614
QY 422 CCCCTGCTTACCTGATGCTGCTGATGACACCCGCC 461
DB 615 CCCCTGCTTACCTGATGCTGCTGATGACACCCGCC 654

RESULT 13
CF726195 750 bp mRNA linear EST 09-OCT-2003
LOCUS
DEFINITION
UI-M-G20-cj-p-h-06-0-UI.r1 NIH_BMAP_G20 Mus musculus cDNA clone
IMAGE:30606413 5', mRNA sequence.

ACCESSION
CF726195
VERSION
CF726195.1 GI:37600363

KEYWORDS
EST.
Mus musculus (house mouse)

SOURCE
ORGANISM
Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: sgabbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
Seq primer: PYX-5.
Location/Qualifiers
1..750

ORIGIN

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30606413"
/tissue_type="whole eye"
/dev_stage="embryo 12.5, 13.5, 14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_G20"
/note="Organ: Eye; Vector: pYX-Absc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Absc vector. The library tag sequence located between the Not I site and the polyA tail is TTAATGAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

Query Match 70.3%; Score 329.2; DB 6; Length 750;
Best Local Similarity 90.5%; Pred. No. 7.8e-83;
Matches 342; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 91 GAGACCAATGGGAGAGTNTCTGTTGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCT 150
DB 1 GAGACCAATGGGAGAGTNTCTGTTGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 151 GACACGAGTTACAGATCTGATGCTTGGATACCTAGTGTCTGCTGCTGCTGCTGCTGCT 210
DB 61 GACACGAGTTACAGATCTGATGCTTGGATACCTAGTGTCTGCTGCTGCTGCTGCTGCT 120
QY 211 NCNCAATGGCCATGACATGCGAAGCCCTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 270
DB 121 GCGCATGGCCATGACATGCGAAGCCCTTTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 271 TTTTNTTGAATGCCAAAAGACAGGCGAGCTATGATGCTGCTGCTGCTGCTGCTGCTGCT 330
DB 181 TTTTNTTGAATGCCAAAAGACAGGCGAGCTATGATGCTGCTGCTGCTGCTGCTGCTGCT 239
QY 331 AATTCAAGGATCTTNAAGCTTGTCAATNTCCAGGACATGACAGCTGACAGCTGAC 390
DB 240 AATTCAAGGATCTTNAAGCTTGTCAATNTCCAGGACATGACAGCTGACAGCTGACAGCTG 299
QY 391 TTGGTAGCTGAGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450
DB 300 TTGGTAGCTGAGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
QY 451 NCACACCCGCCCTCATGG 468
DB 360 TCACACCCGCCCTCATGG 377

RESULT 14
B1738314 628 bp mRNA linear EST 20-SEP-2001
LOCUS
DEFINITION
60336153P1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5368788 5',
mRNA sequence.

ACCESSION
B1738314
VERSION
B1738314.1 GI:15715314

KEYWORDS
EST.
Mus musculus (house mouse)

SOURCE
ORGANISM
Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: sgabbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
Seq primer: PYX-5.
Location/Qualifiers
1..628

THIS PAGE BLANK (USP 10)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:26:08 ; Search time 162 Seconds
(without alignments)
5135.178 Million cell updates/sec

Title: US-10-327-713-267

Perfect score: 468
Sequence: 1 gacgcagcgcgcctcagtg.....ngncacaccgcctcctcagtg 468

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2_6/prodata/1/ina/1.COMB.seq:*
2: /cgn2_6/prodata/1/ina/5.COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/1/ina/H.COMB.seq:*
6: /cgn2_6/prodata/1/ina/PCTUS.COMB.seq:*
7: /cgn2_6/prodata/1/ina/PP.COMB.seq:*
8: /cgn2_6/prodata/1/ina/RE.COMB.seq:*
9: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51.8	11.1	1647	US-09-902-540-4211	Sequence 4211, Ap
2	51.8	11.1	21330	US-09-902-540-1209	Sequence 1209, Ap
3	46.4	9.9	1743	US-09-902-540-4073	Sequence 4073, Ap
4	46.4	9.9	24602	US-09-902-540-1202	Sequence 1202, Ap
5	40.8	8.7	9164	US-09-814-915A-80	Sequence 80, Appl
6	40	8.5	1959	US-09-061-764A-8	Sequence 40, Appl
7	40	8.5	2061	US-09-061-764A-17	Sequence 17, Appl
8	36.8	7.9	897	US-09-303-518D-37	Sequence 37, Appl
9	36.8	7.9	1272	US-09-489-039A-2685	Sequence 2685, Ap
10	36.2	7.7	1812	US-09-583-110-1526	Sequence 1526, Ap
11	36.2	7.7	1848	US-09-107-433-495	Sequence 495, Ap
12	36.2	7.7	7760	US-08-961-527-63	Sequence 63, Appl
13	35	7.5	921	US-09-902-540-5880	Sequence 5880, Ap
14	35	7.5	9574	US-09-902-540-1043	Sequence 1043, Ap
15	34.8	7.4	1800	US-09-252-991A-2972	Sequence 2972, Ap
16	34.8	7.4	2133	US-09-252-991A-2716	Sequence 2716, Ap
17	34.8	7.4	165651	US-09-949-016-13032	Sequence 13032, A
18	34.6	7.4	601	US-09-949-002-1787	Sequence 1787, Ap
19	34.6	7.4	601	US-09-949-002-5940	Sequence 5940, Ap
20	34.6	7.4	33821	US-09-949-002-613	Sequence 613, Appl
21	34.6	7.4	33822	US-09-949-002-737	Sequence 737, Appl
22	34.4	7.4	1168	US-09-227-357-137	Sequence 137, Appl
23	34.4	7.4	1168	US-09-973-278-143	Sequence 143, Appl
24	34.2	7.3	1266	US-09-252-991A-10804	Sequence 10804, A

25	34.2	7.3	1443	3	US-09-252-991A-10228	Sequence 10228, A
26	34.2	7.3	1818	3	US-09-252-991A-10345	Sequence 10345, A
27	34.2	7.3	1974	3	US-09-902-540-8140	Sequence 8140, Ap
28	34.2	7.3	4213	3	US-09-711-619-8	Sequence 8, Appl
29	34.2	7.3	6189	3	US-09-902-540-754	Sequence 754, Appl
30	34.2	7.3	6827	3	US-09-711-619-7	Sequence 7, Appl
31	34.2	7.3	8450	3	US-09-902-540-834	Sequence 834, Appl
32	33.8	7.2	1800	3	US-09-489-039A-5879	Sequence 5879, Ap
33	33.6	7.2	1995	3	US-09-902-540-9307	Sequence 9307, Ap
34	33.6	7.2	10092	3	US-09-902-540-994	Sequence 994, Appl
35	33.6	7.2	13637	3	US-09-902-540-1097	Sequence 1097, Ap
36	33.4	7.1	219	3	US-09-107-532A-3135	Sequence 3135, Ap
37	33.4	7.1	601	3	US-09-949-016-157317	Sequence 157317, Ap
38	33.4	7.1	753	3	US-09-758-759-86	Sequence 86, Appl
39	33.4	7.1	2486	3	US-09-949-016-4392	Sequence 4392, Ap
40	33.4	7.1	12061	3	US-09-949-016-16134	Sequence 16134, A
41	33.4	7.1	109519	3	US-09-758-759-1	Sequence 1, Appl
42	33.2	7.1	808	3	US-09-902-540-8803	Sequence 8803, Appl
43	33.2	7.1	1272	3	US-09-902-540-6825	Sequence 6825, Ap
44	33.2	7.1	4407	3	US-09-902-540-569	Sequence 569, Appl
45	33.2	7.1	5552	3	US-08-155-888-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-902-540-4211
Sequence 4211, Application US/0902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 4211
LENGTH: 1647
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-4211

Query Match	11.1%	Score 51.8;	DB 3;	Length 1647;
Best Local Similarity	44.0%	Pred. No. 1.8e-05;		
Matches 181;	Conservative	0;	Mismatches 229;	Indels 1;
			Gaps	1;
QY	53	CTGGGCGAGCTGGTGGAGATTGTCGCAATACGAGGACCAATGAGGAGTNTGNTG	112	
DB	19	CTGGCCTTATCCCGCGCCGATTTGGCGACTGTGACCAAGCCCTTCAACGGCGCGACCGG	78	
QY	113	TNTGANTCCGNAAGCTCAGNCANCTCTCTACTGNAACGATTTCAAGNACTGNTG	172	
DB	79	TATGTGTGACCGGCTCGGATGCTGATCTCGCCGTGTCACGGTGCAGGGCATGCC	138	
QY	173	ACCTTNGAATACCTAGTCTGTCTCTCCACATTTGNNANCAATGGCATGNAATGCGG	232	
DB	139	ATGCGCTGCGCATCTTCAACCAAGCGCGCAACGCGTGTGTGCGGCTGCGC	198	
QY	233	AAAGCCCTTTTACGCTCCGCTCCGCGCAAGACATCTTTTNTGATGCAAAAGACA	292	
DB	199	AAGGACCTTTCGCGCCCTCTCTCTCCAGAGTGGGCTTTCGATTTGCGCGGACG	258	
QY	293	GGGAGCGTAGTGTGCTTGAATGTCGAAAGATTTCAAGGATCTTNAAGCT	352	
DB	259	GGGAGGTCAC-AGCGGCTCTCTCGACACCAACGCTCTGACGACCAACCTGACGGC	317	
QY	353	TGTGATTTTCCAGGAGCTGACGACTGACCAAGTATTTGTAGCTGAGAGTCTGNN	412	

```

Db      318 CAACGTGTCATGATGATGCTGCTACAGTGTGACAGGCGCCCTGGCGGAGTGGCTGCTGCT 377
QY      413 TATGCTGNCCTCGCTGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463
Db      378 CTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428

```

RESULT 2

```

US-09-902-540-1209/c
; Sequence 1209, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Barry S.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1209
; LENGTH: 21330
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; NAME/KEY: unsure
; LOCATION: (1)..(21330)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1209

```

```

Query Match      11.1%; Score 51.8; DB 3; Length 21330;
Best Local Similarity 44.0%; Pred. No. 5.3e-05;
Matches 181; Conservative 0; Mismatches 229; Indels 1; Gaps 1;

```

```

QY      53 CTGGGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 112
Db      18612 CTGGGCTATCCCGCGCCGCTTGGCGAGCTGATGATGATGATGATGATGATGATGATGATGAT 18553
QY      113 TATGATCCCGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 172
Db      18552 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 18493
QY      173 ACTTNGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 232
Db      18492 ATGGGCGTGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 18433
QY      233 AAGGCGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292
Db      18432 AAGGAGCTTTCGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18373
QY      293 GGGGAGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 352
Db      18372 GGGGAGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 18314
QY      353 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 412
Db      18313 CAACGTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 18254
QY      413 TATGCTGNCCTCGCTGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463
Db      18253 CTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18203

```

```

RESULT 3
US-09-902-540-4073
; Sequence 4073, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

```

```

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4073
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4073

```

```

Query Match      9.9%; Score 46.4; DB 3; Length 1743;
Best Local Similarity 48.5%; Pred. No. 0.0078;
Matches 127; Conservative 0; Mismatches 134; Indels 1; Gaps 1;

```

```

QY      206 GNNGANCNATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 265
Db      265 GATGAGCCATTTGTCAGGACCTGCGGAGCGGCTGTATGCGAGCTTGTGAGAGCAGAG 324
QY      266 ATTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 325
Db      325 ATGCGTTCTTGA-CCAGACCGGACCTGCGGCGCTCACAGCGCGGCTGTGCACTGACAC 383
QY      326 GCAAGATTCAGGATCTTCTTAAAGCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 385
Db      384 GCGCTCATTCAGGCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 443
QY      386 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 445
Db      444 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503
QY      446 TANNNCACACCGCGCTCATG 467
Db      504 GCGGCTGCTCCCGCGGTGACG 525

```

RESULT 4

```

US-09-902-540-1202
; Sequence 1202, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1202
; LENGTH: 24602
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1202

```

```

Query Match      9.9%; Score 46.4; DB 3; Length 24602;
Best Local Similarity 48.5%; Pred. No. 0.0024;
Matches 127; Conservative 0; Mismatches 134; Indels 1; Gaps 1;

```

```

QY      206 GNNGANCNATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 265
Db      7290 GATGAGCCATTTGTCAGGACCTGCGGAGCGGCTGTATGCGAGCTTGTGAGAGCAGAG 7349
QY      266 ATTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 325

```

Db 7350 ATCGGCTTCTTGA-CCAGCACCGCATGCGGCTCTACACACCGGCTGTCCATGACAC 7408
Qy 326 GGAAGATTCAAGCATCTTNAAGCTTATNTNCCAGGACATGAGCTGNACCA 385
Db 7409 CCGCTCATCCAGGGGCGGCTCATGACGACATCGCATCATGCTCCGACAGCAACAC 7468
Qy 386 GGTGATTGTTAGCTTGAAGNCCCTGNNATGTGNCCTCCCTGCTTACCTTATGCTGC 445
Db 7469 GTTGAATTGAGGGCTGCGCTGCTCTACACCTGCGCCGGTGAACCTGCTCATGCT 7528
Qy 446 TGNNGACACCCCGCTCATG 467
Db 7529 GCGGCTGTCCTCCCGGTGACG 7550

RESULT 5
US-09-814-915A-80
; Sequence 80, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; PRIOR FILING DATE: 2002-03-21
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 9164
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-80

Query Match 8.7%; Score 40.8; DB 3; Length 9164;
Best Local Similarity 43.8%; Pred. No. 0.078;
Matches 126; Conservative 0; Mismatches 162; Indels 0; Gaps 0;
Qy 8 CTGAGCTTATGTCGCGACATGATGTCAGATCCCTTCTCTGCGCCAGCTGTC 67
Db 6523 CTGAGCCAGTGGGTGATGAGACCTGGAACCACTGGTGCCTTCTGCTGCGC 6582
Qy 68 GAGATTGTCCCAAGTACAGAGGACCAATGAGGAGNNTGNTGANTCCGNAAG 127
Db 6583 CTGACAGACCCCAAGACCTTCTGCTGGAAGGGGAGCCTGAGAGACAGGACTTCAG 6642
Qy 128 CTGANGNCANCTGCTCTACTGNAAGATTGAGNACTGNTGACTTNGATACCTA 187
Db 6643 GAGCGGCTGATGACCTGACCTGAGCTGAGCTTCTGAGACCCCGGCTTCAG 6702
Qy 188 GTGCTGCTGCCCATTTGNNANCATGCGCATGCAATGCGAAAGCCTTTTCA 247
Db 6703 GCCTTGTGGGTCCACAGGGGTCTCAGGTTTCTGACAAAGTGGGGAACAGGAGC 6762
Qy 248 TCCCTGCTCCGCAAGACATTTCTTTTGTATGCCAAAAGACAGG 295
Db 6763 CCGAGGCCCAAGTCAAGATGTGTCAGTGAAGAAATGAGACAGAG 6810

RESULT 6
US-09-061-764A-4
; Sequence 4, Application US/09061764A
; Patent No. 6284879
; GENERAL INFORMATION:
; APPLICANT: Faustman, Denise L
; TITLE OF INVENTION: TRANSPORT ASSOCIATED PROTEIN SPLICE VARIANTS
; TITLE OF INVENTION: AND MODEL FOR IMMUNE DIVERSITY
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Yankwich & Associates

STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,764A
FILING DATE: April 16, 1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Yankwich, Leon R
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: MGH-002.0 US/MHG-1247.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1959 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: synthetic DNA fragment
US-09-061-764A-4

Query Match 8.5%; Score 40; DB 3; Length 1959;
Best Local Similarity 59.8%; Pred. No. 0.07;
Matches 61; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Qy 198 CCCAATTGNNGNCATGCGCATGATGCGAAAGCCTTTTCACTCTCTGTC 257
Db 644 CTTACACATGCTCCATCACTTCCGATCCGGAGACGCTTCTCTCTCTGTC 703
Qy 258 GCGAAGACATGCTTTTGTATGCGCAAAAGACAGGCGAC 299
Db 704 GCCAGACCTCGGTTCTTCCAGAGACTTAAGACAGGAGC 745

RESULT 7
US-09-061-764A-17
; Sequence 17, Application US/09061764A
; Patent No. 6284879
; GENERAL INFORMATION:
; APPLICANT: Faustman, Denise L
; TITLE OF INVENTION: TRANSPORT ASSOCIATED PROTEIN SPLICE VARIANTS
; TITLE OF INVENTION: AND MODEL FOR IMMUNE DIVERSITY
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,764A
FILING DATE: April 16, 1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

RESULT 9
US-09-489-039A-2685

0y TCANCCANCTGCTCTACTAGNACNGAGTTTACAGNACTGTGACCTTNGATACCTAG 188
Db TCATGGTAACTTGGCGCTGCTGGTTTGGTTCTATTATCTCAAGTGAATATACAGT 307
0y TGCTGCTGCCAATTGNNNCAATGGCCATGACATGGGGAAGCCCTTTTCAGCT 248

Db 308 GTCTCATGACGCGCTGATGAGATGACCAAGATGCGCAAGGCTCTTGTA 367
QY 249 CCTCTCCGGCAGACATGCTTTTGTATGCCAAAAGACAGGCGAGCTAGT 308
Db 368 AGCTGCTCAGTTGACGGTTCTTCTTGA -CGTCGACAAAGATGGGATTCCTGCT 426
QY 309 CGCTTACTAGTGTGCAAGATTCAGAGCATCTTNAAGCTTGTCATNTNCAAGGA 368
Db 427 CATTTACAGATGATTGATATATCTTACAGCCTTTACGAAAGCTTGATTCAGGTC 486
QY 369 CTGAGCA 375
Db 487 ATGAGCA 493

RESULT 11
US-09-107-433-495
; Sequence 495, Application US/09107433
; Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 495:
SEQUENCE CHARACTERISTICS:
LENGTH: 1848 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1848
SEQUENCE DESCRIPTION: SEQ ID NO: 495:
US-09-107-433-495

Query Match 7.7%; Score 36.2; DB 3; Length 1848;
Best Local Similarity 46.6%; Pred. No. 0.95; Mismatches 115; Conservative 0; Mismatches 131; Indels 1; Gaps 1;

QY 129 TCANCGNCANCTGCTCTACTGNAACGATTCAGAGACTGNTGACTTNGGATACCTAG 188
Db 284 TCATGCTAATCTTGGCTGCTGCTGTTTGTATTTATCTCTAGTAAATATACAT 343
QY 189 TGCTGCTGCCACATTGNNANNCNATGCGCATGATGCGGAAGCCCTTTCACT 248
Db 344 GTCTCATACCGCGCTGATTCAGAAATGACCAAGATGCGAAAGGCTCTTGGA 403
QY 249 CCTGCTCCGGCAGACATGCTTTTGTATGCAAAAAGACAGGCGAGCTAGT 308
Db 404 AGCTTGCTCAGTTGACGGTTCTTCTTGA -CGTCGACAAAGATGGGATTCCTGCT 462
QY 309 CGCTTACTAGTGTGCAAGATTCAGAGCATCTTNAAGCTTGTCATNTNCAAGGA 368
Db 463 CATTTACAGATGATTGATATATCTTACAGCCTTTACGAAAGCTTGATTCAGGTC 522
QY 369 CTGAGCA 375
Db 523 ATGAGCA 529

RESULT 12
US-08-961-527-63
; Sequence 63, Application US/08961527
; Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunesh
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 7760 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-63

Query Match 7.7%; Score 36.2; DB 3; Length 7760;
Best Local Similarity 46.6%; Pred. No. 1.8; Mismatches 115; Conservative 0; Mismatches 131; Indels 1; Gaps 1;
QY 129 TCANCGNCANCTGCTCTACTGNAACGATTCAGAGACTGNTGACTTNGGATACCTAG 188
Db 568 TCATGCTAATCTTGGCTGCTGCTGTTTGTATTTATCTCTAGTAAATATACAT 343
QY 189 TGCTGCTGCCACATTGNNANNCNATGCGCATGATGCGGAAGCCCTTTCACT 248

DB 5718 GTCTCATGACGCGCGTGAATTGACGAATGCACCAAGATGGCAAGGCTCTTTGGTA 5777
QY 249 CCTGCTCCGCGAACAACATGCTTTTGTGATGCCAAAAAGACGGGACGGTATGAGT 308
DB 5778 AGCTTGCTCAGTGAAGCGTTCTTTCTTTGA-CCGTGCAACAAGATGGGATATCTGTCT 5836
QY 309 CGCTTGACTACTGATGATGCAAGATTTCAAGGATCTTNAAGCTTGATATNTCCAGGGA 368
DB 5837 CATTTTACCAAGTATTTGATATATCTCCCAAGCTTTAAGAAAGCTTATTCAGGTC 5896
QY 369 CTGNGCA 375
DB 5897 ATGAGCA 5903

RESULT 13
US-09-902-540-5880
; Sequence 5880, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5880
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5880

Query Match 7.5%; Score 35; DB 3; Length 921;
Best Local Similarity 50.7%; Pred. No. 1.6;
Matches 68; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 31 GAATGTGAGATCCCTTGTCTCTGCGCCAGCTGTGTGAGATTGTCCCAAGTACACGAG 90
DB 243 GAGAGT 302
QY 91 GAGACCATGTGGGAGATNTGTTGANTCCGNAAGCTCANCANCCANCTGCTCTACT 150
DB 303 GGAGCAGCGCTGT 362
QY 151 GNAAGAGTTTCAAG 164
DB 363 CCAATTCGGTTTCGG 376

RESULT 14
US-09-902-540-1043/C
; Sequence 1043, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1043
; LENGTH: 9574
; TYPE: DNA

; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(9574)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1043

Query Match 7.5%; Score 35; DB 3; Length 9574;
Best Local Similarity 50.7%; Pred. No. 4.5;
Matches 68; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 31 GAATGTGAGATCCCTTGTCTCTGCGCCAGCTGTGTGAGATTGTCCCAAGTACACGAG 90
DB 5507 GAGGT 5448
QY 91 GAGACCATGTGGGAGATNTGTTGANTCCGNAAGCTCANCANCCANCTGCTCTACT 150
DB 5447 GAGACGAGCGCTGT 5388
QY 151 GNAAGAGTTTCAAG 164
DB 5387 CCAATTCGGTTTCGG 5374

RESULT 15
US-09-252-991A-2972
; Sequence 2972, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2972
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2972

Query Match 7.4%; Score 34.8; DB 3; Length 1800;
Best Local Similarity 48.1%; Pred. No. 2.5;
Matches 75; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 130 CAGCAGCAGCTGCTCTACTGACAGGATTCAGGATCTGATGACCTTNGATACCTAGT 189
DB 234 CATCTGT 293
QY 190 GCTGCTGTCCACATTTGNNGANCATGCGCATGACATGCGGAAAGCCTTTTCAAGTCT 249
DB 294 CCGTGTGTCTGATTCGGGAGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 353
QY 250 CCGTGTCCGGAAGAACATTTGTTTGTGATGCCAA 285
DB 354 CCGATTCGATGTGATTCGCCGGTTTCTACGAAACCAA 389

Search completed: January 20, 2006, 22:25:29
Job time : 165 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: January 20, 2006, 20:33:00 ; Search time 657 Seconds
(without alignments)
5890.516 Million cell updates/sec

Title: US-10-327-713-267

Sequence: 1 gactgagctgcttagctg.....ngmcacccgcctcatcg 468

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: /cgn2_6/ptodaca/1/pubpna/us07_PUBCOMB.seq:*
2: /cgn2_6/ptodaca/1/pubpna/us08_PUBCOMB.seq:*
3: /cgn2_6/ptodaca/1/pubpna/us09_PUBCOMB.seq:*
4: /cgn2_6/ptodaca/1/pubpna/us10_PUBCOMB.seq:*
5: /cgn2_6/ptodaca/1/pubpna/us10B_PUBCOMB.seq:*
6: /cgn2_6/ptodaca/1/pubpna/us10C_PUBCOMB.seq:*
7: /cgn2_6/ptodaca/1/pubpna/us10D_PUBCOMB.seq:*
8: /cgn2_6/ptodaca/1/pubpna/us10E_PUBCOMB.seq:*
9: /cgn2_6/ptodaca/1/pubpna/us10F_PUBCOMB.seq:*
10: /cgn2_6/ptodaca/1/pubpna/us11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	316	67.5	2392	US-10-108-260A-258	Sequence 258, App
2	316	67.5	2417	US-09-823-245A-601	Sequence 601, App
3	219.6	46.9	1805	US-10-264-237-516	Sequence 516, App
4	206.8	44.2	494	US-09-918-995-30941	Sequence 30941, A
5	127.8	27.3	423	US-10-079-623-212	Sequence 212, App
6	127.8	27.3	423	US-10-263-828-64	Sequence 64, App
7	117.6	25.1	425	US-09-918-995-34259	Sequence 34259, A
8	93	19.9	2379	US-11-097-143-2507	Sequence 2507, App
9	93	19.9	4940	US-11-097-143-2506	Sequence 2506, App
C 10	74	15.8	283	US-09-764-891-2676	Sequence 2676, App
C 11	74	15.8	283	US-10-091-572-214	Sequence 214, App
C 12	55.4	11.8	574	US-10-264-237-718	Sequence 718, App
C 13	51.8	11.1	1773	US-10-369-493-43142	Sequence 43142, A
C 14	46.4	9.9	1773	US-10-369-493-43123	Sequence 43123, A
C 15	44	9.4	434	US-10-357-930-30101	Sequence 30101, A
C 16	44	9.4	483	US-10-357-930-45584	Sequence 45584, A
C 17	40.8	8.7	607	US-10-123-155-344	Sequence 344, App
C 18	40.8	8.7	607	US-10-146-731-344	Sequence 344, App
C 19	40.8	8.7	607	US-10-140-472-344	Sequence 344, App
C 20	40.8	8.7	607	US-10-141-761-344	Sequence 344, App
C 21	40.8	8.7	607	US-10-142-885-344	Sequence 344, App
C 22	40.8	8.7	607	US-10-158-790-344	Sequence 344, App
C 23	40.8	8.7	607	US-10-137-871-344	Sequence 344, App

C 24	40.8	8.7	607	US-10-140-923-344	Sequence 344, App
C 25	40.8	8.7	607	US-10-141-755-344	Sequence 344, App
C 26	40.8	8.7	607	US-10-141-753-344	Sequence 344, App
C 27	40.8	8.7	607	US-10-140-805-344	Sequence 344, App
C 28	40.8	8.7	607	US-10-140-864-344	Sequence 344, App
C 29	40.8	8.7	9104	US-10-741-600-799	Sequence 799, App
C 30	40.8	8.7	9164	US-10-776-827-80	Sequence 80, App
C 31	40.8	8.7	9272	US-10-723-860-1784	Sequence 1784, App
C 32	40.8	8.7	9272	US-10-956-157-343	Sequence 343, App
C 33	40.8	8.7	9277	US-10-741-600-801	Sequence 801, App
C 34	40.8	8.7	9287	US-09-960-706-633	Sequence 633, App
C 35	40.8	8.7	9287	US-09-873-319-396	Sequence 396, App
C 36	40.8	8.7	9456	US-10-723-860-6147	Sequence 6147, App
C 37	40.2	8.6	455	US-09-918-995-208	Sequence 208, App
C 38	39.6	8.5	3450	US-10-027-632-116105	Sequence 116105, App
C 39	39.6	8.5	3450	US-10-027-632-116105	Sequence 5383, App
C 40	38	8.1	1352	US-10-739-930-5383	Sequence 11, App
C 41	37.2	7.9	70	US-10-957-432-11	Sequence 802745, App
C 42	37	7.9	506	US-09-925-065A-802745	Sequence 802745, App
C 43	37	7.9	506	US-09-925-065A-802815	Sequence 802815, App
C 44	37	7.9	537	US-09-925-065A-805460	Sequence 805460, App
C 45	37	7.9	614	US-09-925-065A-857856	Sequence 857856, App

ALIGNMENTS

RESULT 1
US-10-108-260A-258
; Sequence 258, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 2392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-258

Query Match 67.5%; Score 316; DB 6; Length 2392;
Best Local Similarity 78.9%; Pred. No. 7.1e-96;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

Qy	5	GACCTGCTTGAAGTGGGCACTAGTGAATGCAATCCCTTCTCTGGCCAGCTG	64
Db	428	GTGCTGGCTTGGGTGGGCACTGCGAATGTAAGATCCCTCTCTGGGCGACCTG	487
Qy	65	GTGGAATTTTCCCAAGTACAGAGGAGCACATGGGGAGNTNMTNTGANTCCCN	124
Db	488	GTAAGGTCTGTGCGCAAGTACAGAGGAGCACATGGAGGTTTCATGACTGCTCCAG	547
Qy	125	AAGCTCANCNCANCTGCTCTACTGNAGGAGTTTCAGNACTGNTGACTTNGATAC	184
Db	548	AATTCAGACACCACTGCTTATCTCTATGATGATCAGGAGCTGACCTTGAGGATC	607
Qy	185	CTAAGTGTGTGTCCTCCCATTTGNNANCATGGCCATGNAATCGGAAAGCCCTTTTC	244
Db	608	CTGATGTGCTGTCCTCCACGTGGCGAGCGGATGCTGTGACATGCGAGGCGCTCTTC	667
Qy	245	AGCTCCCTGCTTCCGAGACATTTCTTTTNTTGTATGCAAAAGACAGGGCAGCTAGT	304
Db	668	AGCTCCCTGCTTCCGAGACATTCCTTTTGACCCATATAGACAGGGCAGC-TGGT	726
Qy	305	GAGTGGTGAATGATGTAAGTAATCAAGGACCTTNAAGCTTGATNTNCCA	364
Db	727	GAGCCGTTTGAACATGACGTGACGAGGTTTAAGTATCTTCAAGCTTGATCTCCA	786

QY 365 GGGAGCTGAGCAGTGNACCCAGGATGTTGTAGCCTGAGAGCCCTGNNATGCTGAGCC 424
DB 787 GGGGCTGGAGAGCTGACCCAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
QY 425 TCGGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
DB 847 ACGGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890

RESULT 2

US-09-823-245A-601
; Sequence 601, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agoetino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulikote, Kamalakr
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 601
; LENGTH: 2417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-601

Query Match 67.5%; Score 316; DB 3; Length 2417;

Best Local Similarity 78.9%; Pred. No. 7, 1e-96;
Matches 366; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 5 GAGCTGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 64
DB 453 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 512
QY 65 GTGAGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 124
DB 513 GTAGAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
QY 125 AAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 184
DB 573 AATCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 632
QY 185 CTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
DB 633 CTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
QY 245 AGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
DB 693 AGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 751
QY 305 GAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
DB 752 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
QY 365 GGGAGCTGAGCAGTGNACCCAGGATGTTGTAGCCTGAGAGCCCTGNNATGCTGAGCC 424
DB 812 GGGGCTGGAGAGCTGACCCAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
QY 425 TCGGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 468
DB 872 ACGGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915

RESULT 3

US-10-264-237-516

; Sequence 516, Application US/10264237

; Publication No. US20040009491A1

; GENERAL INFORMATION:

; APPLICANT: Bires et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA131P1

; CURRENT APPLICATION NUMBER: US/10/264,237

; PRIOR FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/16450

; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/205,515

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 2876

; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 516

; LENGTH: 1805

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (254)..(254)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (313)..(313)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (427)..(427)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (430)..(430)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1803)..(1803)

; OTHER INFORMATION: n equals a,t,g, or c

; US-10-264-237-516

Query Match 46.9%; Score 219.6; DB 6; Length 1805;

Best Local Similarity 75.8%; Pred. No. 2, 9e-63;

Matches 263; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

QY 122 CGAAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 181
DB 1 CAGATCTCAGACACCACTGCTTATCTTATGATGATGATGATGATGATGATGATGATGATG 60
QY 182 TACCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
DB 61 TACCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 242 TTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
DB 121 TTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 179
QY 302 AGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
DB 180 GGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 239
QY 362 CCAAGGAGCTGAGCAGTGNACCCAGGATGTTGTAGCCTGAGAGCCCTGNNATGCTGAG 421
DB 240 CCAAGGAGCTGAGCAGTGNACCCAGGATGTTGTAGCCTGAGAGCCCTGNNATGCTGAG 299
QY 422 CCCTGAGCTTACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
DB 300 GACATGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346

RESULT 4

```
US-09-918-995-30941
; Sequence 30941, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30941
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(494)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30941

Query Match          44.2%; Score 206.8; DB 3; Length 494;
Best Local Similarity 80.1%; Pred. No. 3.7e-59;
Matches 229; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 5 GAGCTGCGCTTACGTGCGGACCTAGTGAATGTCAGATCCCTTGTCTCCGCGCCAGCTG 64
DB 208 GTGCTGCGCTTGTGGTGGCGGACCTCGTGAATGTCAGATCCCTTGTCTCCGCGCCAGCTG 267
QY 65 GTGGAATGTCGCGCAAGTACAGAGGACCACTGCGGAGANTGTCGTTGATGATCCG 124
DB 268 GTGAGAGTGTGCGCAAGTACAGAGGACCACTGCGGAGANTGTCGTTGATGATGATCCG 327
QY 125 AAGCTCAGCAGCAGCTGCTCTACTGACGAGTTCAGGAGTTCAGTTCGTTGATGATGATC 184
DB 328 AATCTGAGCAGCAGCAGCTGCTCTACTGATGATGATGATGATGATGATGATGATGATGATC 387
QY 185 CTGAGTGTGCTGTCGCGCAATGTCGAGTTCAGTTCGAGTTCAGTTCGAGTTCAGTTCGAGT 244
DB 388 CTGAGTGTGCTGTCGCGCAATGTCGAGTTCAGTTCGAGTTCAGTTCGAGTTCAGTTCGAGT 447
QY 245 AGCTCCCTGCTCGCGCAAGCATGTCGTTTGTGATGATGATGATGATGATGATGATGATGATG 290
DB 448 AGCTCCCTGCTCGCGCAAGCATGTCGTTTGTGATGATGATGATGATGATGATGATGATGATG 493

RESULT 5
US-10-079-623-212
; Sequence 212, Application US/10079623
; Publication No. US20020169302A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Gligor, Matthew
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; mammary gland and methods for their use.
; FILE REFERENCE: 11000.10463
; CURRENT APPLICATION NUMBER: US/10/079,623
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-623-212

Query Match          27.3%; Score 127.8; DB 5; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32;
Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
```

```
Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 83 TACACGAGGAGACACATGCGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATG 142
DB 1 TACACGAGGAGACACATGCGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATG 60
QY 143 CTCCTACTGACGAGTTCAGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATG 202
DB 61 CTCCTACTGACGAGTTCAGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATG 120
QY 203 ATTGNNAGNCATGCGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATGATG 262
DB 121 ATCGGAGGAGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 263 GACATGCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 289
DB 181 GACATGCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 207

RESULT 6
US-10-263-828-64
; Sequence 64, Application US/10263828
; Publication No. US20030138905A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Gligor, Matthew
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; mammary gland and methods for their use.
; FILE REFERENCE: 11000.104401con
; CURRENT APPLICATION NUMBER: US/10/263,828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Bovine
US-10-263-828-64

Query Match          27.3%; Score 127.8; DB 6; Length 423;
Best Local Similarity 72.5%; Pred. No. 2e-32;
Matches 150; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 83 TACACGAGGAGACACATGCGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATG 142
DB 1 TACACGAGGAGACACATGCGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATG 60
QY 143 CTCCTACTGACGAGTTCAGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATG 202
DB 61 CTCCTACTGACGAGTTCAGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATG 120
QY 203 ATTGNNAGNCATGCGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATGATG 262
DB 121 ATCGGAGGAGGAGTTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 263 GACATGCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 289
DB 181 GACATGCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 207

RESULT 7
US-09-918-995-34259
; Sequence 34259, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
```

```

1 PRIOR APPLICATION NUMBER: US/09/235,076
2 PRIOR FILING DATE: 1999-01-20
3 NUMBER OF SEQ ID NOS: 38054
4 SOFTWARE: FASTSQ for Windows Version 3.0.
5 SEQ ID NO 34259
6 LENGTH: 425
7 TYPE: DNA
8 ORGANISM: Homo sapiens
9 US-09-918-995-34259

```

Query Match	25.1%	Score 117.6	DB 3	Length 425
Best Local Similarity	77.7%	Pred. No. 5.7e-29		
Matches 146	Conservative	0	Mismatches 41	Indels 1
				Gaps 1

Qy	281	GCCAAAAMGACAGGGCAGGGTAGTAGTGCCTTGACTCTACTATGTCACAAATTCAGGC	340
Db	2	GCCAAATAGCAGGGCAGC-TCGTAGCCGCTTGACACTGACGTGCAGAGTTAAGTC	60
Qy	341	ATCCTTNAAGCTTGTCAATNCCAGGAACTGACAGCTGMACCAGTGATTTGGTACCT	400
Db	61	ATCCTTCAAGCTGTATCTCCACAGGGGCTGGAAAGCTGACACCAGGTGGCAGGCTGCT	120
Qy	401	GGAGNCCCTGANTATGCTGACCCCTTGCTTACCTGATGCTGGCTGNNGCACACCCGC	460
Db	121	GGGTGCCCTGTCCATGCTGTGACACAGCCTCAGCTGCTGATGTTGGGCCACACAGC	180
Qy	461	CCTCATGG	468
Db	181	CTTGATGG	188

RESULT 8
US-11-097-143-2507

```

1      Sequence 2507, Application US/111097143
2      Publication No. US20050208558A1
3      GENERAL INFORMATION:
4      APPLICANT: Ventner, J. Craig
5      APPLICANT: et al.
6      TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
7      TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
8      TITLE OF INVENTION: DROSOPHILA GENES.
9      FILE REFERENCE: C0000728
10     CURRENT APPLICATION NUMBER: US/11/097,143
11     CURRENT FILING DATE: 2005-04-04
12     PRIOR APPLICATION NUMBER: 60/157,832
13     PRIOR FILING DATE: 1999-10-05
14     PRIOR APPLICATION NUMBER: 60/160,191
15     PRIOR FILING DATE: 1999-10-19
16     PRIOR APPLICATION NUMBER: 60/161,932
17     PRIOR FILING DATE: 1999-10-28
18     PRIOR APPLICATION NUMBER: 60/164,769
19     PRIOR FILING DATE: 1999-11-12
20     PRIOR APPLICATION NUMBER: 60/173,383
21     PRIOR FILING DATE: 1999-12-28
22     PRIOR APPLICATION NUMBER: 60/175,653
23     PRIOR FILING DATE: 2000-01-12
24     PRIOR APPLICATION NUMBER: 60/184,831
25     PRIOR FILING DATE: 2000-02-24
26     PRIOR APPLICATION NUMBER: 60/191,637
27     PRIOR FILING DATE: 2000-03-23
28     NUMBER OF SEQ ID NOS: 43008
29     SOFTWARE: FastSeq for Windows Version 4.0
30     SEQ ID NO 2507
31     LENGTH: 2379
32     TYPE: DNA
33     ORGANISM: DROSOPHILA
34     OS-11-097-143-2507

```

Query Match	19.9%	Score 93;	DB 10;	Length 2379;
Best Local Similarity	53.8%;	Pred. No. 2.5e-20;		
Matches 179;	Conservative 0;	Mismatches 153;	Indels 1;	Gaps 1

Db 632 TTCTGAAGAAGCTGAGGCAAAACGGGCGACGACATCTGCTGAGCGCTATACATGCTGCACATCT 681

QY 157 CTGATGACCTTNGGATACCTAGTGTGCTGCTGCTGCCACATTGANNANNCATGGCCATGAC 226

Db 682 GGTTCACCTTATATGATACATCTACCTGTTGACCGCGTCGTGAGAGAGATGGCAGCCAAAG 741

QY 227 ATGGGAAAAGCCCTTTTGACGTCCTCGCTCGGCGCAAGACATGTGCTTNTTTGATGCGCAA 286

Db 742 ATGCGCGAGAGATCTTTTACGCGAATTTGTCTGTCAGAGACATGCGATTTCTTCGATGAGAAAT 801

QY 287 AAGACAGGCGACGCTGATGAGTGCCTTGACTACTGATATGCAAGAAATTCAAGGCATCCTT 346

Db 802 CGAAGCGGGCGAGC-TGTCTCAATGCACTAACCGGCGATGTACAGAGACTTCAAGACCTCGTT 860

QY 347 NAAAGCTTGTCAATNCCAGAGGACTGACAGCTGAAACCCAGGTGATTTGGTAGCTTGAAGC 406

Db 861 CAAGCAGTTTCGTCTCCCAAGGAGCTCGAAGTCTGCTGCCAGCTGATTTGGCGGCGAGTATATC 920

QY 407 CCTGANTATGCTGNCCTCTCGGCTTACCTGAT 439

Db 921 GCTCTTCAATGATTTTACCGCACATGAGCGGCAT 953

RESULT 9
US-11-097-143-2506/c

```

? Sequence 2506, Application US/11097143
? Publication No. US20050208558A1
?
? GENERAL INFORMATION:
?   APPLICANT: Venter, J. Craig
?   APPLICANT: et al.
?   TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
?   TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
?   TITLE OF INVENTION: DROSOPHILA GENES.
?   FILE REFERENCE: C1000728
?   CURRENT APPLICATION NUMBER: US/11/097,143
?   CURRENT FILING DATE: 2005-04-04
?   PRIOR APPLICATION NUMBER: 60/157,832
?   PRIOR FILING DATE: 1999-10-05
?   PRIOR APPLICATION NUMBER: 60/160,191
?   PRIOR FILING DATE: 1999-10-19
?   PRIOR APPLICATION NUMBER: 60/161,932
?   PRIOR FILING DATE: 1999-10-28
?   PRIOR APPLICATION NUMBER: 60/164,769
?   PRIOR FILING DATE: 1999-11-12
?   PRIOR APPLICATION NUMBER: 60/173,383
?   PRIOR FILING DATE: 1999-12-28
?   PRIOR APPLICATION NUMBER: 60/175,693
?   PRIOR FILING DATE: 2000-01-12
?   PRIOR APPLICATION NUMBER: 60/184,831
?   PRIOR FILING DATE: 2000-02-24
?   PRIOR APPLICATION NUMBER: 60/191,637
?   PRIOR FILING DATE: 2000-03-23
?   NUMBER OF SEQ ID NOS: 43008
?   SOFTWARE: FastSeq for Windows Version 4.0
?   SEQ ID NO 2506
?   LENGTH: 4940
?   TYPE: DNA
?   ORGANISM: DROSOPHILA
?   US-11-097-143-2506

```

Query Match	Similarity	Score	DB	Length
Best Local	53.84	Pred. No. 3.3e-20		
Matches	179	Conservative	0	Mismatches 153; Indels 1; Gaps 1;

QY	107	TNCNTGTTGANTCCCGNAGCTCAGTCCAGCCAGCTGCTCTCTAGACGATGTTGAGANA	166
DB	3079	TTCCGTAAGGACGTGAGCAAAACCGGCGACATCTGCTAGACCTATATCATGCTGCATCT	3020
QY	167	CTGNTGACCTTGGATACCTAGTCTGCTGTCGCCACATTGNNGANCATGGCCATGNAAC	226
DB	3019	GGTTTACCTTTTATGTATCATCTTACCTCTTTAGACCCGCTCGGTGTAGACAGATGGACGCCAAG	2960

PRIOR FILING DATE: 2000-09-01	PRIOR APPLICATION NUMBER: 60/229,345
PRIOR FILING DATE: 2000-09-01	PRIOR APPLICATION NUMBER: 60/229,287
PRIOR FILING DATE: 2000-09-01	PRIOR APPLICATION NUMBER: 60/229,513
PRIOR FILING DATE: 2000-09-05	PRIOR APPLICATION NUMBER: 60/231,413
PRIOR FILING DATE: 2000-09-08	PRIOR APPLICATION NUMBER: 60/229,509
PRIOR FILING DATE: 2000-09-05	PRIOR APPLICATION NUMBER: 60/236,367
PRIOR FILING DATE: 2000-09-29	PRIOR APPLICATION NUMBER: 60/237,039
PRIOR FILING DATE: 2000-10-02	PRIOR APPLICATION NUMBER: 60/237,038
PRIOR FILING DATE: 2000-10-02	PRIOR APPLICATION NUMBER: 60/237,037
PRIOR FILING DATE: 2000-10-02	PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02	PRIOR APPLICATION NUMBER: 60/240,960
PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/239,935
PRIOR FILING DATE: 2000-10-13	PRIOR APPLICATION NUMBER: 60/239,937
PRIOR FILING DATE: 2000-10-13	PRIOR APPLICATION NUMBER: 60/241,787
PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: 60/246,474
PRIOR FILING DATE: 2000-11-08	PRIOR APPLICATION NUMBER: 60/246,532
PRIOR FILING DATE: 2000-11-08	PRIOR APPLICATION NUMBER: 60/226,681
PRIOR FILING DATE: 2000-11-08	PRIOR APPLICATION NUMBER: 60/249,216
PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/225,755
PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/225,213
PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/227,162
PRIOR FILING DATE: 2000-08-22	PRIOR APPLICATION NUMBER: 60/225,214
PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-27	PRIOR APPLICATION NUMBER: 60/230,438
PRIOR FILING DATE: 2000-09-06	PRIOR APPLICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-06-30	PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/249,218
PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249,212
PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249,207
PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249,245
PRIOR FILING DATE: 2000-11-17	PRIOR APPLICATION NUMBER: 60/249,244

1	PRIOR APPLICATION NUMBER: 60/249,217
2	PRIOR FILING DATE: 2000-11-17
3	PRIOR APPLICATION NUMBER: 60/249,211
4	PRIOR FILING DATE: 2000-11-17
5	PRIOR APPLICATION NUMBER: 60/249,215
6	PRIOR FILING DATE: 2000-11-17
7	PRIOR APPLICATION NUMBER: 60/249,265
8	PRIOR FILING DATE: 2000-11-17
9	PRIOR APPLICATION NUMBER: 60/249,214
10	PRIOR FILING DATE: 2000-11-17
11	PRIOR APPLICATION NUMBER: 60/249,297
12	PRIOR FILING DATE: 2000-11-17
13	PRIOR APPLICATION NUMBER: 60/232,400
14	PRIOR FILING DATE: 2000-09-14
15	PRIOR APPLICATION NUMBER: 60/231,242
16	PRIOR FILING DATE: 2000-09-08
17	PRIOR APPLICATION NUMBER: 60/233,081
18	PRIOR FILING DATE: 2000-09-08
19	PRIOR APPLICATION NUMBER: 60/232,080
20	PRIOR FILING DATE: 2000-09-08
21	PRIOR APPLICATION NUMBER: 60/231,414
22	PRIOR FILING DATE: 2000-09-08
23	PRIOR APPLICATION NUMBER: 60/231,244
24	PRIOR FILING DATE: 2000-09-08
25	PRIOR APPLICATION NUMBER: 60/233,063
26	PRIOR FILING DATE: 2000-09-14
27	PRIOR APPLICATION NUMBER: 60/233,397
28	PRIOR FILING DATE: 2000-09-14
29	PRIOR APPLICATION NUMBER: 60/232,359
30	PRIOR FILING DATE: 2000-09-14
31	PRIOR APPLICATION NUMBER: 60/232,401
32	PRIOR FILING DATE: 2000-09-14
33	PRIOR APPLICATION NUMBER: 60/241,808
34	PRIOR FILING DATE: 2000-10-20
35	PRIOR APPLICATION NUMBER: 60/241,826
36	PRIOR FILING DATE: 2000-10-20
37	PRIOR APPLICATION NUMBER: 60/241,786
38	PRIOR FILING DATE: 2000-10-20
39	PRIOR APPLICATION NUMBER: 60/241,221
40	PRIOR FILING DATE: 2000-10-20
41	PRIOR APPLICATION NUMBER: 60/246,475
42	PRIOR FILING DATE: 2000-11-08
43	PRIOR APPLICATION NUMBER: 60/231,243
44	PRIOR FILING DATE: 2000-09-08

Query Match	15.8%	Score 74;	DB 5;	Length 283;
Best Local Similarity	77.6%	Pred. No. 2.9e-14;		
Matches 97;	Conservative 1;	Mismatches 26;	Indels 1;	Gaps 1

OY	242	TTTCAGCTCCTCTGCTCCGGCAAGACATTGCTTTNTTGAATGCCAAAAAGACAGGGCAACGT	302
Db	219	TTCTTGCCCATATCCAGACAAACATVACCTTCTTTGACGCCAATAGACACAGGGCAAC-T	161
OY	302	AGTGAATCGTTGACTGATATGTGCAGAAATTCAAGGCATCCTTNAAGCTTGTCAATTN	361
Db	160	GGTAGACCGCTTGACCAACTNAGTGCAGGAGTTTAAGTCATCCCTTCAAGCTTGTCAATTC	101
OY	362	CCAGG	366
Db	100	CCAGG	96

RESULT 12-237-718
US-10-264-237-718
; Sequence 718, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Bire et al.,
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAL31P1
; CURRENT APPLICATION NUMBER: US/10/264,237

```

; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 718
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (454)..(454)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (523)..(523)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-718

```

```

Query Match      11.8%; Score 55.4; DB 6; Length 574;
Best Local Similarity 71.9%; Pred. No. 7.6e-08;
Matches 82; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

```

```

OY 5 GAGCTGCTTAGTGGCGGCACTAGTGAATGTCAGATCCCTTGTCTCTGGGCGCACTG 64
    |||
Db 460 GTGTGGCTTGGTGGCGGCACTGTGAATGTCAGATCCCTTGTCTCTGGGCGCACTG 519
    |||
OY 65 GTGAGATTGTG-CGCCAATGACAGAGGACCAATGGGAGNTGNTGTA 117
    |||
Db 520 GTAAAGTCGTGGGCAAGTACACAGGAGACAGTAAGGAGTTCATGATTGA 573
    |||

```

```

RESULT 13
US-10-369-493-43142
; Sequence 43142, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 43142
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-10-369-493-43142

```

```

Query Match      11.1%; Score 51.8; DB 6; Length 1773;
Best Local Similarity 44.0%; Pred. No. 2e-06;
Matches 181; Conservative 0; Mismatches 229; Indels 1; Gaps 1;

```

```

OY 53 CTGGGCGCGTGTGGAGATTGTGGCCAAAGTACACAGAGGACCAATGGGAGNTGNTG 112
    |||
Db 196 CTGGCTATATCCCCCGCCATTTGGGACCTGTGTGACCAAGGCCCTTACCGCGCGACCGG 255
    |||
OY 113 TATGATNTCCGAAAGCTCAGNCANCTGCTCTACTAGTACAGAGTTCAGAGTCTGNTG 172
    |||
Db 256 TATGATGAGGACCGGCTCGCATGTGTATGCTCGCGATTCACAGGTGCAAGGCGATCGCC 315
    |||
OY 173 ACCTTGGATACCTAGTGTCTGTGTCCCAATGNNANNCATGAGCCATGACATGCGG 232
    |||
Db 316 ATGGCGCTGCGCATCTACTCTTACCAACAGCCGCGAAGCGGTGTGTGCGGCTGCGC 375
    |||

```

```

OY 233 AAAACCTTTTTCAGCTCCCTGCTCCGGCAAGACATTGCTTTTGTGATGCAAAAAGACA 292
    |||
Db 376 AAGAGCTCTTCCGCGCCCTGTGCTGTCCCAAGAGGTGGGCTTCTTCACTGCGCCGACAG 435
    |||
OY 293 GGGCAGCGTAGTGAAGTGGCTTGACTATGATGNCAGAAATTCAGAGCATCTTNAAGCT 352
    |||
Db 436 GGGAGCTCACCC-AGCCGGCTCTCTCGAGACACACCGCTCTCGAGACCAACCTCACGGC 494
    |||
OY 353 TGTCAATNTCCAGGGACTGAGCACTGNAACCAAGTATTGTAGCTTGAGNCCCTGNN 412
    |||
Db 495 CAAGTGTCCATGATGCTGGGCTAGCTGTCACAGGCGCTGGGGGGGCTGGCTGCTGCT 554
    |||
OY 413 TATGTCNCCCTCGCTTACCTTATGCTGTGCTGNNANNCACACCCGCCCT 463
    |||
Db 555 CTACACGTCCGTTCACACTCACGCTGTGTGTGTGCGCGTATCCGCCCT 605
    |||

```

```

RESULT 14
US-10-369-493-43123
; Sequence 43123, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 43123
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-10-369-493-43123

```

```

Query Match      9.9%; Score 46.4; DB 6; Length 1773;
Best Local Similarity 48.5%; Pred. No. 0.00013;
Matches 127; Conservative 0; Mismatches 134; Indels 1; Gaps 1;

```

```

OY 206 GNNGANNCATGGCGCATGNAACATGGCGGAAGCCCTTTCAGCTCCCTGCTCCGCAAGAC 265
    |||
Db 301 GGTGAGCGCATGTGTACAGCACTGCGGAGCGGCTGTATGCGACGTTGCGAGCAGAG 360
    |||
OY 266 ATTGCTTTTATGATGCAAAAAGACAGGCGACGTAAGTGTGCTTGACTATGATGT 325
    |||
Db 361 ATGCGGTTCTTGA-CCAGACCGCACTGCGGCGCTCACAGCGGCTGTCACTGACAC 419
    |||
OY 326 GCAAGAAATTCAGGCACTCTTNAAGCTTTCATNTNCCAGGACTGACAGTGNACCA 385
    |||
Db 420 CGCCCTCATCAGGCGCCCTGTAGTACGACATGCACTGATGCTGTGCAACGCAAC 479
    |||
OY 386 GTGATTTGTAGTGTGAGTGGAGCCCTGNNATGATGCTGNCCTTACCTTACCTGATGTG 445
    |||
Db 480 GTTATTTGAGGGGTGGCGCTGCTGTCTTACCTGCGCGGTTGACGCTGTATGCT 539
    |||
OY 446 TANNNCACACCGCCCTCATG 467
    |||
Db 540 GCGGCTGTGCTCCCGCTGACG 561
    |||

```

```

RESULT 15
US-10-357-930-30101
; Sequence 30101, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert

```

```
/ APPLICANT: Endege, Wilson
/ APPLICANT: Monahan, John
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
/ TITLE OF INVENTION: HUMAN PROSTATE CANCER
/ FILE REFERENCE: MRI-007BCN
/ CURRENT APPLICATION NUMBER: US/10/357,930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785,276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211,314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219,007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 30101
/ LENGTH: 434
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-357-930-30101

Query Match          9.4%; Score 44; DB 8; Length 434;
Best Local Similarity 46.3%; Pred. No. 0.00049;
Matches 139; Conservative 0; Mismatches 160; Indels 1; Gaps 1;

QY 140 CTGCTCTACTAGNACNAGATTGACGNACTGNTGACTTNGAIPACTAGTCTGCTGTCC 199
    |||||
DB 55 CTGTTGCGGTGCGCGCGGTGCTCGCGTGGCCACCGCGCGCTTACATGGGTGCC 114
    |||||

QY 200 CACATTGNNGANONCATGGCCCATGNA CATGGCGAAAGCCCTTTGAGCTCCCTGCTCCGG 259
    |||||
DB 115 TGGCTGGGCGAGCGCTGACGGCAATTCGCAAGCGGCTCTACCGCCACGTGGTGC9C 174
    |||||

QY 260 CAAGACATTGCTTTTGTATGCAAAAAGACAGGGCAGGTAGTGGCTTGAATAC 319
    |||||
DB 175 CAGAGCCCCGAATTCCTGAGACCAACCCGAC- CGCGAAGTGTCTGCGGCTGACAC 233
    |||||

QY 320 TGAATGCAAGAAATTCAGGCAATCTTNAAGCTTGTCAATNCCAAGGACGTGCACTG 379
    |||||
DB 234 CGACACCACTGATCTCAGACCGTGTGCGCACACAGCATCTGCTGGCGCTGCAACAC 293
    |||||

QY 380 NACCCAGGTGATTTGTAAGCTGAGNCCCTGNNNTATGCTGNCCTCCGCTTACCTGAT 439
    |||||
DB 294 GCTGCTGTCTTCTGGCGGCTGGTGTGCTGTTCTGACCAAGCCGCGCTGACCTTCAT 353
    |||||
```

Search completed: January 20, 2006, 22:36:34
Job time : 659 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 20:40:58 ; Search time 242 Seconds
(without alignments)
1594.049 Million cell updates/sec

Title: US-10-327-713-267

Perfect score: 468
Sequence: 1 gactgagctgccttagtg.....ngncacaccgcctcatg 468

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0 .

Searched: 6049916 seqs, 41213615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New: *
1: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq: *
2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq: *
3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq: *
4: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq: *
5: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq: *
6: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq: *
7: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq: *
8: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq: *
9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq: *
10: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq: *
11: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43.8	9.4	4990	US-11-128-061-932	Sequence 932, App
2	43.8	9.4	4990	US-11-128-049-932	Sequence 932, App
3	37.8	8.1	2436	US-11-128-061-368	Sequence 368, App
4	37.8	8.1	2436	US-11-128-049-368	Sequence 368, App
5	36.6	7.7	198265	US-10-775-169-338	Sequence 338, App
6	36.6	7.7	201	US-10-995-561-68215	Sequence 68215, A
7	36.2	7.7	16175	US-10-995-561-13399	Sequence 13399, A
8	35.2	7.5	201	US-10-995-561-68325	Sequence 68325, A
9	35	7.5	2446	US-11-136-527-3071	Sequence 3071, App
10	33.8	7.2	65455	US-11-124-368A-2884	Sequence 2884, App
11	33.6	7.2	5868	US-11-136-527-3354	Sequence 3354, App
12	33.4	7.1	2548	US-11-136-527-1128	Sequence 1128, App
13	33	7.1	1284	US-10-750-185-36207	Sequence 36207, A
14	33	7.1	1284	US-10-750-623-36207	Sequence 36207, A
15	32.8	7.0	1008	US-11-055-822-61	Sequence 61, App1
16	32.6	6.9	3321	US-11-136-527-2646	Sequence 2646, App
17	32.2	6.9	201	US-11-124-368A-5812	Sequence 5812, App
18	32.2	6.9	201	US-11-124-368A-5812	Sequence 5812, App
19	32.2	6.9	201	US-11-124-368A-11173	Sequence 11173, A
20	32.2	6.9	201	US-11-124-368A-11174	Sequence 11174, A
21	32.2	6.9	503	US-11-108-172-878	Sequence 878, App
22	32.2	6.9	4932	US-11-124-368A-63	Sequence 63, App1

C 23	32.2	6.9	168656	US-11-112-908-59	Sequence 59, App1
C 24	32.2	6.9	170285	US-11-112-908-58	Sequence 58, App1
C 25	31.6	6.8	3434	US-11-136-527-1894	Sequence 1894, App
C 26	31.4	6.7	3497	US-11-000-688-1085	Sequence 1085, App
C 27	31.4	6.7	3412	US-11-136-527-2282	Sequence 2282, App
C 28	31.4	6.7	4101	US-10-821-234-579	Sequence 579, App
C 29	31.4	6.7	4749	US-10-821-234-244	Sequence 244, App
C 30	31.4	6.7	4770	US-11-000-463-7	Sequence 7, App1
C 31	31.4	6.7	5086	US-11-186-284-30	Sequence 30, App1
C 32	31.4	6.7	5921	US-11-186-284-29	Sequence 29, App1
C 33	31.4	6.7	6728	US-11-186-284-27	Sequence 27, App1
C 34	31.4	6.7	6728	US-11-021-603-1	Sequence 1, App1
C 35	31.4	6.7	26277	US-10-995-561-13414	Sequence 13414, A
C 36	31.2	6.7	1400	US-11-117-161-10	Sequence 10, App1
C 37	31.2	6.7	1400	US-11-080-251-10	Sequence 10, App1
C 38	31.2	6.7	3453	US-11-136-527-1893	Sequence 1893, App
C 39	30.8	6.6	2026	US-10-750-185-44073	Sequence 44073, A
C 40	30.8	6.6	2026	US-10-750-623-44073	Sequence 44073, A
C 41	30.8	6.6	4791	US-11-000-463-479	Sequence 479, App
C 42	30.6	6.5	3901	US-10-821-234-112	Sequence 112, App
C 43	30.6	6.5	4276	US-11-136-527-4010	Sequence 4010, App
C 44	30.6	6.5	5460	US-11-186-284-32	Sequence 32, App1
C 45	30.6	6.5	6264	US-11-075-185-58	Sequence 58, App1

ALIGNMENTS

RESULT 1	
US-11-128-061-932	
Sequence 932, Application US/11128061	
General Information:	
APPLICANT: Melville, Mark W.	
APPLICANT: Charlebois, Timothy S.	
APPLICANT: Mounts, William M.	
APPLICANT: Hann, Louane E.	
APPLICANT: Sinacore, Martin S.	
APPLICANT: Leonard, Mark W.	
APPLICANT: Brown, Eugene L.	
APPLICANT: Miller, Christopher P.	
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS	
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION	
FILE REFERENCE: 01997.027701	
CURRENT APPLICATION NUMBER: US/11/128,061	
CURRENT FILING DATE: 2005-05-11	
PRIOR APPLICATION NUMBER: US 60/570,425	
PRIOR FILING DATE: 2004-05-11	
NUMBER OF SEQ ID NOS: 7285	
SOFTWARE: PatentIn version 3.3	
SEQ ID NO 932	
LENGTH: 4990	
TYPE: DNA	
ORGANISM: Cricetus griseus	
FEATURES:	
NAME/KEY: misc feature	
LOCATION: (4888) ..(4948)	
OTHER INFORMATION: n is a, c, g, or t	
US-11-128-061-932	
Query Match	9.4% Score 43.8; DB 8; Length 4990;
Best Local Similarity	46.2% Pred. No. 0.0017;
Matches 108; Conservative	0; Mismatches 126; Indels 0; Gaps 0;
DB	1407 GAGAGGCTTATGTCGAGGACATGTCAGATCCCTTGCTCTGAGGCACTG 64
QY	5 GAGCTGAGCTTATGTCGAGGACATGTCAGATCCCTTGCTCTGAGGCACTG 64
DB	1407 GAGAGGCTTATGTCGAGGACATGTCAGATCCCTTGCTCTGAGGCACTG 1466
QY	65 GTGAGATTGTGCGCAATGACAGAGGACCAATGCGGAGGAGTNTGATCCCGN 124
DB	1467 GTCTCTCCGCTTCTCCGAGACAGGTGCTCCCTCCGAGGAGTTCCTGCTGCTCCAG 1526
QY	125 AAGCTCAGCAGCAGCTGCTCTACTGACAGGATTCAGGACGATGACCTTGATAC 184

DB 1527 GAAATACGGGTCCCAAGGTGACCTGGAGAGACTGGATCCAAAGGGGAACGGGCTTC 1586
QY 185 CTAGTCTGCTGCTCCCACTTNNNANNCATGGCCATGACATGGGAAAGCC 238
DB 1587 CTGGAGAACGTGGCTTACGAGAGAACTGGAGGCTTGGCCGAATGCAAGAGAGAC 1640

RESULT 2

US-11-128-049-932
Sequence 932, Application US/11128049
Publication No. US20060010513A1

GENERAL INFORMATION:

APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
TITLE OF INVENTION: MAKING AND USING SAME
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 932
LENGTH: 4990
TYPE: DNA
ORGANISM: Cricetus griseus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (4888)..(4948)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-932

Query Match 9.4%; Score 43.8; DB 8; Length 4990;
Best Local Similarity 46.2%; Pred. No. 0.0017;
Matches 108; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 5 GAGCTGCGCTTAGTGGCGGCACTAGTGAATGTGACATCCCTTCTCTGGGCCAGCTG 64
DB 1407 GAGAAAGCCCTATGTCTCCCAAGGTGACCGTGGAGCTCTGTGATCTTGACTTGGG 1466
QY 65 GTGAGATTTGTGCGCAAGTACAGAGGACCAATGGGGAGTNCNTGTTGANTCCCGN 124
DB 1467 GTCTCCCGGTCTTCCAGAGAGGTGCTGCTCCCTGGCCAGGGTTTCCCTGTGTCCAG 1526
QY 125 AAGCTCAGCAGCAGCTGCTCTACTGACGAGTTCAGGACGAGTTCAGTTCCTTNGATAC 184
DB 1527 GAAATACGGGTCCCAAGGTGACCGTGGAGAGACTGTGATCCAAAGGGGAACAGGGGCTTC 1586
QY 185 CTAGTCTGCTGCTCCCACTTNNNANNCATGGCCATGACATGGGAAAGCC 238
DB 1587 CTGGAGAACGTGGCTTACGAGAGAACTGGAGGCTTGGCCGAATGCAAGAGAGAC 1640

RESULT 3

US-11-128-061-368

Sequence 368, Application US/11128061
Publication No. US20060003958A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.

APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 368
LENGTH: 2436
TYPE: DNA
ORGANISM: Mesocricetus auratus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (820)..(837)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1544)..(1544)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-368

Query Match 8.1%; Score 37.8; DB 8; Length 2436;
Best Local Similarity 52.4%; Pred. No. 0.094;
Matches 54; Conservative 1; Mismatches 48; Indels 0; Gaps 0;

QY 215 ATGGCATGACATGCGGAAAGCCCTTTCACTCTCTCTCGGCAAGACTTCTTNN 274
DB 738 ATCAACTCGGATACGAGAGAGCTTTCTCTCTCTCGGCAAGACTTCTTNN 797
QY 275 TTTATGCCAAAAGACAGGCGACGCTGATGCTGCTTACT 317
DB 798 TTCCAGAGAACAGACAGGAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840

RESULT 4

US-11-128-049-368

Sequence 368, Application US/11128049
Publication No. US20060010513A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
TITLE OF INVENTION: MAKING AND USING SAME
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 368
LENGTH: 2436
TYPE: DNA
ORGANISM: Mesocricetus auratus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (820)..(837)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1544)..(1544)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-368

Query Match 8.1%; Score 37.8; DB 8; Length 2436;
Best Local Similarity 52.4%; Pred. No. 0.094;
Matches 54; Conservative 1; Mismatches 48; Indels 0; Gaps 0;

QY 215 ATGGCCATGACATGCGGAAAGCCCTTTTCACTCCCTGCTCGGCAACATGCTT 274
DB 738 ATCAACCTGGGATACGAGAGGCTTTCTCTCTGCTGCGCAACCTTGAGTT 797

QY 275 TTGTATGCCAAAAGACAGGCGAGCTAGTGAAGTCTGCTGACT 317
DB 798 TTCCAGAGAACACAGACAGGRRNNNNNNNNNNNNNNNGCT 840

RESULT 5
US-10-775-169-338
; Sequence 338, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dornier, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities in Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 338
; LENGTH: 198285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-338

Query Match 7.8%; Score 36.6; DB 7; Length 198285;
Best Local Similarity 58.8%; Pred. No. 2.1;
Matches 57; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 198 CCCACATTGNNGANCATGCGCATGACATGCGGAAAGCCCTTTTCACTCCCTGCTCC 257
DB 118712 CCTACACCATGCTCTCAATCACTTGGGATCGGGAGCAGCTTTCTCTCTGCTGC 118771

QY 258 GGCAGACATGCTTTTNTTGTATGCCAAAAGACAG 294
DB 118772 GCCAGACCTCGGTTCTTCCAGAGACTTAAGACAG 118808

RESULT 6
US-10-995-561-68215
; Sequence 68215, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: Carigill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68215
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-68215

Query Match 7.7%; Score 36.2; DB 7; Length 201;
Best Local Similarity 57.7%; Pred. No. 0.085;
Matches 56; Conservative 1; Mismatches 40; Indels 0; Gaps 0;

QY 198 CCCACATTGNNGANCATGCGCATGACATGCGGAAAGCCCTTTTCACTCCCTGCTCC 257

DB 87 CCTACACCATGCTCTCAATCACTTGGGATCGGGAGCAGCTTTCTCTCTGCTCC 146

QY 258 GGCAGACATGCTTTTNTTGTATGCCAAAAGACAG 294
DB 147 GCCAGACCTCGGTTCTTCCAGAGACTTAAGACAG 183

RESULT 7
US-10-995-561-13399
; Sequence 13399, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: Carigill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13399
; LENGTH: 16175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13399

Query Match 7.7%; Score 36.2; DB 7; Length 16175;
Best Local Similarity 57.7%; Pred. No. 0.78;
Matches 56; Conservative 1; Mismatches 40; Indels 0; Gaps 0;

QY 198 CCCACATTGNNGANCATGCGCATGACATGCGGAAAGCCCTTTTCACTCCCTGCTCC 257
DB 15156 CCTACACCATGCTCTCAATCACTTGGGATCGGGAGCAGCTTTCTCTCTGCTGC 15215

QY 258 GGCAGACATGCTTTTNTTGTATGCCAAAAGACAG 294
DB 15216 GCCAGACCTCGGTTCTTCCAGAGACTTAAGACAG 15252

RESULT 8
US-10-995-561-68325
; Sequence 68325, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: Carigill, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68325
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-68325

Query Match 7.5%; Score 35.2; DB 7; Length 201;
Best Local Similarity 62.7%; Pred. No. 0.18;
Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 212 CNGATGGCATGACATGCGGAAAGCCCTTTTCACTCCCTGCTCGGCAACATGCT 271
DB 8 CGAATCAACTTGGGATCGGGAGCAGCTTTCTCTCTGCTGCGCAGACCTGGT 67

QY 272 TTTTGTATGCCAAAAGACAG 294
DB 68 TTCTTCCAGAGACTTAAGACAG 90

RESULT 9
US-11-136-527-3071
Sequence 3071, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3071
LENGTH: 2446
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-3071

Query Match
Best Local Similarity 62.4%; Score 35; DB 8; Length 2446;
Pred. No. 0.72;
Matches 53; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 215 ATGGCCATGACATGCGGAAGCCCTTTTCACTCCCTCGGCAAGACATTCCTTN 274
DB 750 ATCAACCTGCGCATGAGAGAGAGAGCTTTCTCATCTTGTGCGTCAGACCTTGCAATTC 809
QY 275 TTTGATGCCAAAAGACAGGCGCAGC 299
DB 810 TTCCAGAGACCAAGACAGGCGGAGC 834

RESULT 10
US-11-124-368A-2884/C
Sequence 2884, Application US/11124368A
Publication No. US20050287559A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 2112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2884
LENGTH: 65455
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-368A-2884

Query Match
Best Local Similarity 7.2%; Score 33.8; DB 8; Length 65455;
Pred. No. 9.1;
Matches 50; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 267 TTGCTTTNTTGTATGCAAAAAGACAGGCGAGTAGTGCTGCTTGACTAATGATG 326
DB 10263 TTTTCTTTTGTGTAAGCTCAGGAGAGCTAGTGTGCTTGAATTAATGTT 10204
QY 327 CAGAATTCAGGCAATCC 344
DB 10203 AAAAGTGAATGAAACC 10186

RESULT 11
US-11-136-527-3354
Sequence 3354, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3354
LENGTH: 5868
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc feature
LOCATION: (5416)..(5416)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (5439)..(5439)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (5858)..(5858)
OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-3354

Query Match
Best Local Similarity 7.2%; Score 33.6; DB 8; Length 5868;
Pred. No. 3.1;
Matches 57; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 8 CTGGCTTAGGTTGGGACACTAGTGAATGCAATCCCTTGTCTCTGGCCAGCTGTG 67
DB 1589 CTGGAGTCTTGGGACAGCCCTGTCTGTATGCAAAACCGGCCCCCTGTGTCTC 1648
QY 68 GAGATTTGCCAAGTACACAGAGGACCAATGGGG 103
DB 1649 AAGATGTGCGCCCTGGAACCGCAAGTCTCTCTGGAG 1684

RESULT 12
US-11-136-527-2128
Sequence 2128, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2128
LENGTH: 2548
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-2128

Query Match
Best Local Similarity 7.1%; Score 33.4; DB 8; Length 2548;
Pred. No. 2.4;
Matches 64; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 65 GTGAGATTTGTGCGCAAGTACACAGAGGACCAATGGGAGTNTGTTTGAATCCCGN 124

Db 1266 GTGGCTACTGTGGCTACCAAGCAAGAGCTTAGAAGAAATTTGTAGATTTTGT 1325
QY 125 AAGCTCAGCAGCAGCAGCTCTCTACTGACAGAGTTCAGGAGTCTTGAAGCTTGAATAC 184
Db 1326 CATCCGAGAGCAACAACACTTCTTAAGAGACAGCTTTCAAGAGGTGTGAATTAAGGC 1385
QY 185 CTAGTCTGT 193
Db 1386 CAAGTCTGT 1394

RESULT 13
US-10-750-185-36207/c
; Sequence 36207, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent version 3.1
; SEQ ID NO 36207
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Bovine 19866881290303
US-10-750-185-36207

Query Match 7.1%; Score 33; DB 7; Length 1284;
Best Local Similarity 50.7%; Pred. No. 2.2;
Matches 72; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 238 CCTTTTCACTCCCTGCTCCGCAAGACATTGCTTTTGTGATGCCAAAAGACAGGGCA 297
Db 554 CCTTTTCACTCCATTTTCTGTCAAGAAAGCCTTCTTGGAAACAAATCGACATGGGG 495
QY 298 GCGTAGTAGTCCGCTTACTAGTAGTGCAAGAAATCAAGGACCTTAAAGCTTGTCA 357
Db 494 CCAGGAGTCAAGGATGTGTATATGGGAGGAGCAGCAGACACTGTGTTAGCTTGGCC 435
QY 358 TTTTCCAGGAGTCTGAGGCTG 379
Db 434 CTTCACAGAGAACACTGACTG 413

RESULT 14
US-10-750-623-36207/c
; Sequence 36207, Application US/10750623
; Publication No. US2005028753A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: Patent version 3.1
; SEQ ID NO 36207
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Bovine 19866881290303
US-10-750-623-36207

Query Match 7.1%; Score 33; DB 7; Length 1284;
Best Local Similarity 50.7%; Pred. No. 2.2;
Matches 72; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 238 CCTTTTCACTCCCTGCTCCGCAAGACATTGCTTTTGTGATGCCAAAAGACAGGGCA 297
Db 554 CCTTTTCACTCCATTTTCTGTCAAGAAAGCCTTCTTGGAAACAAATCGACATGGGG 495
QY 298 GCGTAGTAGTCCGCTTACTAGTAGTGCAAGAAATCAAGGACCTTAAAGCTTGTCA 357
Db 494 CCAGGAGTCAAGGATGTGTATATGGGAGGAGCAGCAGACACTGTGTTAGCTTGGCC 435
QY 358 TTTTCCAGGAGTCTGAGGCTG 379
Db 434 CTTCACAGAGAACACTGACTG 413

RESULT 15
US-11-055-822-61
; Sequence 61, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 61
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(985)
; OTHER INFORMATION: RXC00733
US-11-055-822-61

Query Match 7.0%; Score 32.8; DB 8; Length 1008;
Best Local Similarity 45.3%; Pred. No. 2.3;

